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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Dec 4 16:03:31 1997; MasPar time 8.83 Seconds 614.595 Million cell updates/sec Ilar output not generated.

>US-08-790-043A-1 (1-256) from US08790043A.pep 1753 1 MINIENKTYVIMGIANKRSI.......LSSGVTGENIHVDSGFHAIK 256

Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

59021 seqs, 21210388 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

swiss-prot34 Database:

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11

Mean 49.533; Variance 114.207; scale 0.434 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	3.73e-125	2.09e-104	1.39e - 101	4.06e-99	1.29e-38	2.64e - 37	7.37e-35	4.16e-17	1.65e-16	1.29e-15	9.16e-16	7.07e-15	2.12e-12	2.07e-10	7.54e-10	1.97e-09	9.64e-09	9.64e-09	1.81e-08	2.48e-08	3.40e-08	4.64e-08
Description	PUTATIVE ENOYL-[ACYL-	ENOYL-[ACYL-CARRIER-P	ENOYL-[ACYL-CARRIER-P	ENOYL-[ACYL-CARRIER-P	ENOYL-[ACYL-CARRIER P	ENOYL - [ACYL - CARRIER - P	ENOYL-[ACYL-CARRIER-P	7-ALPHA-HYDROXYSTEROI	7-ALPHA-HYDROXYSTEROI	ADIPOCYTE P27 PROTEIN	TROPINONE REDUCTASE-I	TROPINONE REDUCTASE-I	NODULATION PROTEIN G	HYPOTHETICAL OXIDORED	7-ALPHA-HYDROXYSTEROI	HYPOTHETICAL OXIDORED	GLUCONATE 5-DEHYDROGE	3-OXOACYL-[ACYL-CARRI	HYPOTHETICAL OXIDORED	TROPINONE REDUCTASE H	NODULATION PROTEIN G.	D-ARABINITOL 2-DEHYDR
ID	FABI ANASP	FABI_ECOLI	FABI_SALTY	FABI_HAEIN	FABI_BRANA	INHA MYCSM	INHA MYCTU	BA71_EUBSP	BA72 EUBSP		TRN2 HYONI	TRN2 DATST	NODG RHIME	YJGU_ECOLI	HDHA_ECOLI	YXAU BACSU	GNO_GLUOX	FABG_CUPLA	YJGI ECOLI	TRNH_DATST	NODG AZOBR	ARDH_PICST
DB		٣	m	m	m	ß	'n	-	Н	Н	σ	σ	ø	급	4	11	4	m	11	σ	ø	Н
Length	264	261	261	261	385	269	269	249	249	244	260	260	245	254	255	262	256	320	261	268	246	278
% Query Match	49.3	42.7	41.8	41.0	20.8	20.4	19.5	13.1	12.8	12.5	12.5	12.2	11.2	10.4	10.2	10.0	8.6	8	9.6	9.6	5	9.5
Score	865	748	732	718	365	357	342	229	225	219	220	214	197	183	179	176	171	171	169	168	167	166
Lt.	-	10	m	4	· ru	9	7	. 00	σ.	10	11	12	1.5	14	15	16	17	80	19	20	21	22

8.66e-08	1.18e-07	1.18e-07	1.61e-07	4.07e-07	1.02e-06	1.02e-06	1.02e-06	1.38e-06	1.38e-06	2.54e-06	3.43e-06	2.54e-06	2.54e-06	6.26e-06	1.14e - 05	1.53e-05	1.53e-05	2.78e-05	1.20e-04	1.20e-04	1.61e-04	2.15e-04	
3-OXOACYL-[ACYL-CARRI	2,5-DICHLORO-2,5-CYCL	VERSICOLORIN REDUCTAS	FIXE PROTEIN.	SPORULATION PROTEIN S	HYPOTHETICAL OXIDORED	HYPOTHETICAL OXIDORED	2,5-DICHLORO-2,5-CYCL	TROPINONE REDUCTASE-I	D-ARABINITOL 2-DEHYDR	3-OXOACYL-[ACYL-CARRI	2-DEOXY-D-GLUCONATE 3	7-ALPHA-HYDROXYSTEROI	D-ARABINITOL 2-DEHYDR	HYPOTHETICAL OXIDORED	3-OXOACYL-[ACYL-CARRI	ACETOACETYL-COA REDUC	HYPOTHETICAL OXIDORED	PUTATIVE OXIDOREDUCTA	ACETOACETYL-COA REDUC	PTERIDINE 1 REDUCTASE	GRANATICIN POLYKETIDE	GLINCOSE 1 - DEHYDROGENA	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
FABG_ECOLI	LINX_PSEPA	VER1 ASPPA	FIXR BRAJA	SP19_YEAST	YHXC_BACSU	YHXD BACSU	LINC_PSEPA	TRN1_DATST	ARDH CANAL	FABG_VIBHA	KDUD BACSU	HDHA_CLOSO	ARDH CANTR	YXJF BACSU	FABG HAEIN	PHAB_ACISP	YWFD BACSU	YOZE MYCTU	PHBB ALCEU			DHC BACME	DEG 2000
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244	250	256	278	295	114	140	250	273	281	244	254	267	282	257	242	248	255	247	246	289	249	261	101
4.6	6.9	6.3	6	9.1	6.8	0.0	6	8	8	8.7	8.7	8.7	8.7	9, 8	4	8.4	8.4	000	0	0 0	0 1		۲.
164	163	163	162	159	156	156	156	155	155	153	152	153	153	150	148	147	147	145	140	140	130	0 0	100
23	24	25	26	27	28	60	30	31	3.5	9.6	34	П	9	3.7	α,	o 6	0.4	7 7	C 7	7 7			0.4

ALIGNMENTS

PHEDELICAL PROTEIN; OXIDOREDUCTASE; NAD; FATTY ACID BIOSYNTHESIS. NP BIND 10 36 NAD (BY SIMILARITY). SEQUENCE 264 AA; 28083 MW; A78ADCBB CRC32; t Local Similarity 51:6%; Pred. t Local Similarity 51:6%; Pred. T minitgknalvtaiannrsiawqiaqqlaaqanlqitylpd-ergkfekkvselvepln 65

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STRAIN-K12 / W3110;

FRUITGER S., HUGHES G.J., PASQUALI C., HOCHSTRASSER D.F.;

FURITIOER S., HUGHES G.J., PASQUALI C., HOCHSTRASSER D.F.;

SUBMITTED (FEB-1996) TO THE SWISS-PROT DATA BANK.

-!- CATALYTIC ACTIVITY: ACYL-[ACYL-CARRIER PROTEIN] + NAD(+) =

TRANS-2, 3-DEHYDROACYL-[ACYL-CARRIER PROTEIN] + NADH.

-!- PATHWAY: SECOND REDUCTIVE STEP IN FATTY ACID BIOSYNTHESIS.

-!- THE ANTHEIOTIC DIAZABORINE INTERFERES WITH THE ACTIVITY BY BINDING
                                                                                                                                                                                                                                                                                                                                                                                                  ESCHERICHIA COLI.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M97219; G145851; -.

PIR; X78733; G587106; -.

PIR; A47681.

ECCOGENE: EG11528; FABI.

OXIDOREDUCTASE; NAD; FATIY ACID BIOSYNTHESIS; ANTIBIOTIC RESISTANCE; INIT_MET MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 lsgkrilvtgvasklsiaygiagamhregaelaftygndklkgrveefaaglg-sdivl- 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 94164884.
BERGLER H., WALLNER P., EBELING A., LEITINGER B., FUCHSBICHLER S., ASCHAUER H., KOLLENZ G., HOEGERAUER G., TURNOWSKY F.; J. BIOL. CHEM. 269:5493-5496(1994).
                                                                                                                                                                                                                      01-DEC-1992 (REL. 24, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE (NADH) (EC 1.3.1.9) (NADH-DEPENDENT ENOYL-ACP REDUCTASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAD (BY SIMILARITY).
G->S: DIAZABORINE RESISTANCE.
S->F: PRODUCES TEMPERATURE-SENSITIVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE: 9435561
KATER M.M., KONINGSTEIN G.M., NIJKAMP H.J.J., STUITJE A.R.;
PLANT MOL. BIOL. 25:771-790(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: INNER MEMBRANE-ASSOCIATED.
-!- SIMILARITY: SOME SIMILARITY TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES FAMILY (SDR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBMITTED (OCT-1994) TO THE SWISS-PROT DATA BANK
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Pred. No. 2.09e-104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND SEQUENCE OF 1-30. MEDLINE; 93123967.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BERGLER H., HOEGENAUER G., TURNOWSKY F.,
J. GEN. MICROBIOL. 138:2093-2100(1992).
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                                                                                                                                                                              PRT;
238 SSGVTGENIHVDSGFHAI 255
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Matches 111; Conservative
                                                                                                                                                                              STANDARD;
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STRAIN-K12 / EMG2;
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P29132;
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J. BACTERIOL. 171:6555-6565(1989).
-!- CATALYLIC ACTIVITY: ACYL-[ACYL-CARRIER PROTEIN] + NAD(+) =
TRANS-2,3-DEHYDROACYL-[ACYL-CARRIER PROTEIN] + NADH.
-!- PATHWAY: SECOND REDUCTIVE STEP IN FATTY ACID BIOSYNTHESIS.
-!- THE ANTIBIOTIC DIAZABORINE INTERFERES WITH THE ACTIVITY BY BINDING
TO THE PROTEIN.
61 qcdvaedasidtmfaelgkvwpkfdgfvhsigfapgdqldgdyvnavtregfkiahdiss 120
                 121 ysfvamakacrsmlnpgsalltlsylgaeraipnynvmglakasleanvrymanamgpeg 180
                                                                            181 vrvnaisagpirtlaasgikdfrkmlahceavtpirrtvtiedvgnsaaflosdlsagis 240
                                                                                                                                         PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
ENTEROBACTERIACEAE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OXIDOREDUCTASE; NAD; FATTY ACID BIOSYNTHESIS; ANTIBIOTIC RESISTANCE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                         01-AUG-1990 (REL. 15, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNORATION UPDATE)
ENOXL-[ACYL-CARRIER-PROTEIN] REDUCTASE (NADH) (EC 1.3.1.9) (NADH-
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136819D6 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: INNER MEMBRANE-ASSOCIATED.
-!- SIMILARITY: SOME SIMILARITY TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES FAMILY (SDR).
EMBL; M31806; G153955; -.
PIR; B43729; B43729.
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Pred. No. 1.39e-101;
65; Mismatches 71;
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                                                                                                                                                                                                                                                                       261 AA.
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35 NA
92 G-
27629 MW;
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Local Similarity 43.8%;
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243 GENIHVDSGF 252
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                                                                                                                                                                                                                                                      LT 3
FABI_SALTY
P16657;
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NP_BIND
MUTAGEN
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                                                                                                                                                                    CAPPARALES; CRUCIFERAE.
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104
109
109
280
385 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                         TISSUE-SEED;
MEDLINE; 92003700.
                                                                                                                                                                                                                                      STRAIN-CV. RAFAL;
MEDLINE; 92003699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INHA_MYCSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSIT
P80030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 irvnaisagpirtlaasgikníkkmlstfektaalrrtvtiedvgnsaaflosdlasgit 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --- CATALYTIC ACTIVITY: ACYL-[ACYL-CARRIER PROTEIN] + NAD(+) --
TRANS-2,3-DEHYDROROYL-[ACYL-CARRIER PROTEIN] + NADH.
--- PATHWAY: SECOND REDUCTIVE STEP IN FATTY ACID BIOSYN'HESIS.
--- THE ANTIBIOTIC DIAZABORINE INTERFERES WITH THE ACTIVITY BY BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 pldvatdesigncfaelskrwdkfdgfihaiafapgdgldgdyvnaatregyriahdisa 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 ltgkrilvtglasnrsiaygiaksmkeggaelaftylndklgprveefakefg-sdivl- 60\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F., FLEISCHMANN R.D., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M., MCKELNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D., SCOTT J.D., SHIRLEY R., LIU L.T., GLODEK A., KELLEY J.M., WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D., UTTERBACK T.R., HANNA M.C., NGOYEN D.T., SAUDEK D.M., BRANDON R.C., UTTERBACK T.R., HANNA M.C., NGOYEN D.T., GEOGHAGEN N.S.M., GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 41.0%; Score 718; DB 3; Length 261;
Local Similarity 43.2%; Pred. No. 4.06e-99;
nss 108; Conservative 70; Mismatches 69; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SUBCELLULAR LOCATION: INNER MEMBRANE-ASSOCIATED (BY SIMILARITY).
-1- SIMILARITY: SOME SIMILARITY TO THE SHORT-CHAIN
DEHYROGERNAESES/REDOCTASES FAMILY (SDR).
EMBL: 032846; 6926624; ALL INIT.
OXIDOREDUCTASE; NAD; FATTY ACID BIOSYNTHESIS; ANTIBIOTIC RESISTANCE;
                                                                                                                                                                      01-NOV-1995 (REL. 32, CREATED)
01-NOV-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
ENOYL-16ACTI-CARRIER-PROTEIN] REDUCTASE (NADH) (EC 1.3.1.9) (NADH-DEPRUDENT ENOYL-ACP REDUCTASE).
PABI OR ENVM OR HI1734.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0 0 BY SIMILARITY.
9 35 NAD (BY SIMILARITY).
261 AA; 2798 MW; EFEA381B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      385 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCIENCE 269:496-512(1995)
                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                               HAEMOPHILUS INFLUENZAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 geivhydagf 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 GENIHVDSGF 252
                                          :|| :|||:||
242 TGENIHVDSGF 252
                240 sgevvhvdggf 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=RD / KW20;
MEDLINE; 95350630.
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                           PASTEURELLACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INNER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LT 5
FABI_BRANA
                                                                                                                                                 FABI_HAEIN
P44432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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199 dfgsidilvhsla--ngpevskplletsrkgylaaisassysfvsllsh-flpimnpgga 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHLOROPLAST.
ENOYL-[ACYL-CARRIER PROTEIN] REDUCTASE.
01-AUG-1992 (REL. 23, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANOTATION UPDATE)
01-OCT-1996 (REL. 34, LAST ANOTATION UPDATE)
(NACT-1-CARRIER PROPERTY) REDUCTASE (NADH) PRECURSOR (EC 1.3.1.9)
(NADH-DEPENDENT ENOYL-ACP REDUCTASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLABAS A.R., COTIINGHAM I., AUSTIN A., FANCETT I., SIDEBOTTOM C.M.; PLANT MOL. BIOL. 17:911-914(1991).
-!- CATALYTIC ACTIVITY: ACYL-[ACYL-CARRIER PROTEIN] + NAD(+) = 2,3-DEHYDROACYL-[ACYL-CARRIER PROTEIN] + NADH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SUBDITI: HOMOTETRAINE.
-1- PATHWAY: SECOND REDUCTIVE STEP IN FATTY ACID BIOSYNTHESIS.
-1- PATHWAY: SECOND REDUCTIVE STEP IN FATTY ACID BIOSYNTHESIS.
-1- ENZYME REGULATION: IS INACTIVATED BY PHENYLYGLYOXAL BY BINDING COVALENTLY TO TWO ARGININE RESIDUES.
-1- TISSUE SPECIFICITY: SEEDS AND LEAVES.
-1- SUBLIALIAR LOCATION: CHLOROPLAST.
-1- SIMILARITY: SOME SIMILARITY TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES FAMILY (SDR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE (NADH) (EC 1.3.1.9) (NADH-
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 74-122;146-174;181-193;250-295;301-311;316-346;371-385.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    316 aigfidtmieysynnapigktltadevgnaaaflvsplasaitgatiyvdnglnsm 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              250 GVGGFNTILKEIEERAPLKRNVDQVEVGKTAAXLLSDLSSGVTGENIHVDSGFHAI 255
                                                                                                                                                        BRASSICA NAPUS (RAPE).
EUKARYOTA: PLANTA; EMBRYOPHYTA; ANGIOSPERNAE; DICOTYLEDONEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; MYCOBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 20.8%; Score 365; DB 3; Length 385; Local Similarity 38.1%; Pred. No. 1.29e-38; ns 67; Conservative 54; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OXIDOREDUCTASE; NAD; FATTY ACID BIOSYNTHESIS; CHLOROPLAST;
                                                                                                                                                                                                                                                                                                                                                              KATER M.M., KONINGSTEIN G.M., NIJKAMP H.J., STUITJE A.R.; PLANT MOL. BIOL. 17:895-909(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269 AA
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND SEQUENCE OF 74-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MYCOBACTERIUM SMEGMATIS.
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20.4%; Score 357; DB 5; Length 269;
35.4%; Pred. No. 2.64e-37;
vative 59; Mismatches 92; Indels 19; Gaps 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 ISSYSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVONYNYMGVAKASLEANVKYLALDLG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 kvgvrsnlvaagpirtlamsaivggalgdeaggggmglleegwdgraplgwnmkdptpvak 240
                                                                                                                                                                                                                                                                                                                                                                                                62 eldvqneehlstladritaeigegnkidgvvhsigfmpqsgmginpffdapyedvskgih 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 PDNIRVNAISAGPIRTLSAKG-VGG-F-N-T----ILKEI-EERAPLKRNV-DQVEVGK 228
                                                                                                                                                                                                                                                                                                                                        5 legkrilvtgiitdssiafhiakvaqeagaelvlt-gfdrl-klvkriadrlpkp-apll 61
                                                                                                                                                                                                                                                                                                                                                          OXIDOREDUCTASE; NAD; FATTY ACID BIOSYNTHESIS; ANTIBIOTIC RESISTANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CATALTIC ACTIVIT: ACYL-(ACYL-CARRIER PROTEIN) + NAD(+) = TRANS-2, 3-DEHYDROACYL-(ACYL-CARRIER PROTEIN) + NADH.
-!- PATHWAT: SECOND REDOCTIVE STEP IN FATTY ACID BIOSYNTHESIS. THIS ISOZYME IS INVOLVED IN MYCOLIC ACID BIOSYNTHESIS.
-!- INVOLVED IN THE RESISTANCE AGAINST THE ANTITUBERCULOSIS DRUGS ISONIAZID AND ETHIONAMIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: SOME SIMILARITY TO THE SHORT-CHAIN DEHYDROGENASES/REDCTASES FAMILY (SDR).
EMBL: U02492; G407314; -- OXIDOREDUCTASE; NAD; FATTY ACID BIOSYNTHESIS; ANTIBIOTIC RESISTANCE. NP_BIND 136 165 NAD (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE (NADH) (EC 1.3.1.9) (NADH-
                                                                                                                                                                                                               NAD (POTENTIAL),
S -> A (IN INH-RESISTANT STRAIN MC
SQUARED 651),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BANERGEE A., DUBNAU E., QUEMARD A., BALASUBRAMANIAN V., UM K.S. WILSON T., COLLINS D., DE LISLE G., JACOBS W.R. JR.; SCIENCE 263:227-230(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MYCOBACTERIUM TUBERCULOSIS, AND MYCOBACTERIUM BOVIS.
PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; MYCOBACTERIACEAE.
                                                                                                                                              -!- SIMILARITY: SOME SIMILARITY TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES FAMILY (SDR).
                                                                                                                                                                                                                                                          13E0DC4C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         269 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 tvcallsdwlpattgtviyadgg 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229 TAAYLLSDLSSGVTGENIHVDSG 251
                                                                                                                                                                                                                                                      269 AA; 28527 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEPENDENT ENOYL-ACP REDUCTASE).
                                                                                                                                                                                                                                                                                              Local Similarity 35.4%;
les 93; Conservative
                                                                                                                                                                           EMBL; U02530; G437204; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                               165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=H37RV, AND BCG;
MEDLINE; 94112548.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INHA_MYCTU
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Score 342; DB 5; Length 269;
Pred. No. 7.37e-35;
65; Mismatches 93; Indels 19; Gaps 14;
                                                                                                                                                                                             64 QIDVQSDEEVINGFEQIGKDVG--N-IDGVYHSIAFANMEDL-RGRESETSREGFLLAQD 119
                                                                                                                                                                         62 eldvgneehlaslagrvteaigagnkldgvvhsigfmpqtgmginpffdapyadvskgih 121
                                                                                                                                                                                                                                      122 isaysyasmakallpimnpggsivgmdf-dpsrampaynwmtvaksalesvnrfvareag 180
                                                                                                                                                                                                                                                                  120 ISSYSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVONYNVMGYAKASLEANVKYLALDLG 179
                                                                                                                                                                                                                                                                                                    181 kygvrsnlvaagpirtlamsaivggalgeeagagiglleegwdgrapigwnmkdatpvak 240
                                                                                                                                                                                                                                                                                                                       5 ldgkrilvsgiitdssiafhiarvaqeqgaqlvlt-gfdrlrl-iqritdrl-pakapll 61
                                                                                                                                 -1- SIMILARITY: THERE ARE THREE GENES FOR BAIA PROTEINS: BAIAI IS IDENTICAL TO BAIA3 AND THERE IS 81% IDENTITY WITH BAIA2.
     94 94 S -> A (IN INH-RESISTANT STRAIN NZ).
269 AA; 28528 MW; 26DC955E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEOXYCHOLIC ACID AND LITHOCHOLIC ACID, YIELDING AFFINITY WITH TAUROCHENODEOXYCHOLIC ACID, RESPECTIVELY. HIGHEST CATALYTIC ACTIVITY: 3-ALPHA,7-ALPHA,12-ALPHA-TRIHYDROXY-5-BETA-CHOLANATE + NADG(+) = 3-ALPHA,12-ALPHA-TRIHYDROXY-5-BETA-CHOLANATE + NADH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
7-ALPHA-HYDROXYSTEROID DEHYDROGENASE (EC 1.1.1.159) (BILE ACID
7-DEHYDROXYLASE) (7-ALPHA-HSDH) (BILE ACID-INDUCIBLE PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COLEMAN J.P., WHITE W.B., HYLEMON P.B.;
J. BACTERIOL. 169:1516-1521(1987).
-!- FUNCTION: 7-ALPHA-DEHYDROXYLATION OF CHOLIC ACID, YIELDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GOPAL-SRIVASTAVA R., MALLONEE D.H., WHITE W.B., HYLEMON P.B., J. BACTERIOL. 172:4420-4426(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-55 FROM N.A. (BAIA1), AND SEQUENCE OF 1-33 MEDLINE; 87165759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- PATHWAY: BILE ACID METABOLISM.
-!- INDUCTION: PRESENCE OF C(24) BILE ACIDS CONTAINING A 7-ALPHA-HYDROXY GROUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EUBACIERIUM SP. (STRAIN VPI 12708).
PROKARYOTA; FIRMICUTES; IRREGULAR ASPOROGENOUS RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COLEMAN J.P., WHITE W.B., LIJEWSKI M., HYLEMON P.B.;
J. BACTERIOL. 170:2070-2077(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 AA
                                                                                                                                                                                                                                                                                                                                                                 241 tvcallsdwlpattgdiiyadggaht 266
                                                                                                                                                                                                                                                                                                                                                                                               229 TAAYLLSDLSSGVTGENIHVDSGFHA 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1988 (REL. 08, CREATED)
                                                  Query Match
Best Local Similarity 33.5%;
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (BAIA3).
MEDLINE; 90330548.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (BAIA1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M34658; G148522; EMBL; M19654; G148516; EMBL; M15813; G148516; EMBL; M15813; G148514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROPONIBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A28212; A28212
PIR; A26938; A26938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88197993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BAIA1 AND BAIA3.
VARIANT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             BA71_EUBSP
P07914:
                                                Query Match
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Matches
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Score 229; DB 1; Length 249;
Pred. No. 4.16e-17;
80; Mismatches 104; Indels 12; Gaps 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 DISS-YSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKXLALD 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175 iirkniryvgvapgvvdtdmtkglpp-e-iledylktlpmkrmlkpeeianvylflasdl 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WHITE W.B., FRANKLUND C.V., COLEMAN J.P., HYLEMON P.B.;
J. BACTERTOL. 170:4555-4561(1988).

-!- FUNCTION: 7-ALPHA-DEHYDROXXLATION OF CHOLIC ACID, XIELDING
DEOXYCHOLIC ACID AND LITHOCHOLIC ACID. RESPECTIVELY. HIGHEST
AFFINITY WITH TAUROCHENODEOXYCHOLIC ACID.

-!- CATALYTIC ACITUITY: 3-ALPHA, 7-ALPHA, 12-ALPHA-TRIHYDROXY-5-BETA-
CHOLANATE + NAD(+) = 3-ALPHA, 12-ALPHA-DIHYDROXY-7-OXO-5-BETA-
CHOLANATE + NAD(+)
                                                                                                                                                                                                                                                                                                                                                                                                                             58 evlgfapdltsrdavmaavgtvaqkygrldvminnagit-mnsvfsrvseedfkn-imdi 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 nvngvfngawsayqcmk-dakqgviintasvtgiygslsgigyptskagviglthglgre 174
                                                                                                                                                                                                                                                                                                                                                            2 LNL-ENKTYVIMGIANKRSIAFGVARVLDQLGAKL-VFTYRKERSRKELEKLLEQLNQPE 59
                                                                                                                                                                                                                                                                                                                                1 mklvqdkitiitg-gt-rgigfaaaklfiengakvsifgetqeevdtalagl-kelypee 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
7-ALPHA-HYDROXYZIERGID DEHYDROGENASE (EC 1.1.1.159) (BILE ACID
7-DEHYDROXYLASE) (7-ALPHA-HSDH) (BILE ACID-INDUCIBLE PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 90330548.
GOPAL-SRIVASTAVA R., MALLONEE D.H., WHITE W.B., HYLEMON P.B.;
                                                                    OXIDOREDUCTASE; NAD; BILE ACID CATABOLISM; MULTIGENE FAMILY NP_BIND 7 13 NAD (POTENTIAL).
                                                                                          157 137 NAD (POTENTIAL).
157 157 BY SIMILARITY.
159 162 TSKA -> YQGG (IN REF. 2).
249 AA; 26658 MW; 9E49D579 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EUBACTERIUM SP. (STRAIN VPI 12708).
PROKARYOTA; FIRMICUTES; IRREGULAR ASPOROGENOUS RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          249 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 90264339.
MALLONEE D.H., WHITE W.B., HYLEMON P.B.; J. BACTERIOL. 172:3400-3408(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MALLONEE D.H., WHITE W.B., HYLEMON P.B.; J. BACTERIOL. 172:7011-7019(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BACTERIOL. 172:4420-4426(1990).
          PIR; B37762; B37762.
HSSP; P19992; 1HDC.
PROSITE; PS00061; ADH_SHORT.
                                                                                                                                                                                                                                                  Match 13.1%;
Local Similarity 23.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  233 asgitattisvdgayrp 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238 SSGVTGENIHVDSGFHA 254
                                                                                                                                                                                                                                                                                               61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE; 90330548.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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BA72_EUBSP
P19337:
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                                                                                                                                                            ACT_SITE
                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                       Query Match
                                                                                                                                     NP_BIND
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Score 225; DB 1; Length 249;
Pred. No. 1.65e-16;
81; Mismatches 103; Indels 12; Gaps 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 DISS-YSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVONYNYMGVAKASLEANKYLALD 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 iirknirvvgvapgvvntdmtngnpp-e-imegylkalpmkrmlepeeianvylflasdl 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 LGPDNIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVDQVEVGKTAAYLLSDL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAVRE M., RINGOLD G.M.;
J. CELL BIOL. 107:279-286(1988).
-!- INDUCTION: THIS PROTEIN IS INDUCED BY GLUCOCORTICOIDS.
-!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 evlgfapdltsrdavmaavggvaqkygrldvminnagits-nnvfsrvseeefk-himdi 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 mnlvgdkvtiitg-gt-rgigfaaakifidngakvsifgetqeevdtalagl-kelypee 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: THERE ARE THREE GENES FOR BAIA PROTEINS: BAIA1 IS IDENTICAL TO BAIA3 AND THERE IS 81% IDENTITY WITH BAIA2.
-!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                      NAD OR NADP (BY SIMILARITY).
-!- PATHWAY: BILE ACID METABOLISM.
-!- INDUCTION: PRESENCE OF C(24) BILE ACIDS CONTAINING A
7-ALPHA-HYDROXX GROUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.; D8C37C9B CRC32;
                                                                                                                                                                                                                                                                                                       NAD (POTENTIAL).
NAD (POTENTIAL).
BY SIMILARITY.
W, 453C0028 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1988 (REL. 08, CREATED)
01-AUG-1988 (REL. 08, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
ADIPOCYTE P27 PROTEIN (AP27).
                                                                                                                                                                                                                                                                                                                                                                                                          12.8%; Score 225; dest Local Similarity 23.7%; Pred. No. 1 datches 61; Conservative 81; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 AA; 25958 MW;
                                                                                                                                                                                                                                                                                                           7 13 NAJ
32 36 NAJ
157 157 BY
249 AA; 26538 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, D221.3; G699608; -.
EMBL, X07411; G50004; -.
PIR; A28053, A28053.
PIR; S03382; S03382,
PROSITE; PS00061; ADH_SHORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             233 asgitattvsvdgayrp 249
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                                                                                                                             EAMILY (SDR).

EMBL; M36292; G148528; -.

EMBL; M22623; G290676; -.

EMBL; U57489; G1381567; -.
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149
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                                                                                                                                                                                                            PIR; A31841; A31841.
PIR; E37844; E37844.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 88273310.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FAMILY (SDR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OXIDOREDUCTASE.
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AP27_MOUSE
P08074;
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ACT_SITE
SEQUENCE
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SEQUENCE
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Local Similarity 26.7%; Pred. No. 9.16e-16;
les 69; Conservative 72; Mismatches 100; Indels 17; Gaps 15;
                                          61 lgdwdatekalggigpvdllvnnaalvimg-pflevtkeafdrsfsvnlrsvfqvsqmva 119
                                                               74 INGFEQIGKDVGNIDGVTHSIAFANMEDLRGRFSETTSREGFLLAQDISSYSLTIVAH-EA 132
                                                                                         120 rdminrgvpgsivnvssmvahvtfpnlitysstkgamtmltkamamelgphkirvnsvnp 179
                                                                                                         133 KKLMPEG--GSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDNIRVNAISA 190
                                                                                                                                       180 tvvltdmgkkvsadpefarklkerhplrkfaevedvvnsilfilsdrsastsgggilvda 239
                                                                                                                                                      4; Gaps
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUB-CULTURED ROOT;
MEDLINE: 94120000.
NARAJIMA K., HASHIMOTO T., YAMADA Y.;
PLANT PHYSIOL. 103:1465-1466(1993).
-!- FULLION: CATALYSES THE STEREOSPECIFIC REDUCTION OF TROPINONE TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 -easv-cdlssrsereefmktvsnhfhgklnilvnnagiviykea-kdytmedyshimsi 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 YQIDVQSDEEVINGFEQIGKDVGN-IDGVYHS-IAFANMEDLRGRFSETSREGF--LLAQ 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 nfeaayhlsvlahpflk-asergnvvfissisgasalpyeavygatkgamdqltrclafe 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- PATHWAY: BIOSYNTHETIC PATHWAY OF TROPANE AKKALOIDS.
-i- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177 wakdnirvngvgpgviatsmvemtiqdpeqkenldklidrcalrrmgepkelaavvaflc 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- CATALYTIC ACTIVITY: PSEUDOTROPINE + NADP(+) = TROPINONE + NADPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 nlegctalvtg-gs-rgigygiveelanlgas-vytcs--rngkeldecitgwrskgfnv 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 NLENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYRKERSRKELEKLLEQLNQPEAHL 62
                                                                                                                                                                                                                                                                               01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
TROPINONE REDUCTASE-II (E. 11.1.236) (TR-II).
HYOSCYAMUS NIGER (HENBANE)
EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
 Score 219; DB 1; Length 244;
Pred. No. 1.29e-15;
55; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NADP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Y SIMILARITY.
5C7123E5 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 37 N
159 159 B
260 AA; 28437 MW;
Query Match
Best Local Similarity 25.3%;
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FAMILY (SDR).

EMBL, L20485; G425150; OXIDOREDUCTASE; NADP.

NP_BIND

ACT_SITE 159 159
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                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                      240 gy 241
                                                                                                                                                                                                             251 GF 252
                                                                                                                                                                                                                                                            TRN2_HYONI
P50164:
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SEQUENCE
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Pred. No. 7.07e-15;
82; Mismatches 97; Indels 15; Gaps 15;
                                                                                                                                                                                                                                     -!- CATALYTIC ACTIVITY: PSEUDOTROPINE + NADP(+) - TROPINONE + NADPH.
-!- PATHWAY: BIOSYNTHETIC PATHWAY OF TROPANE ALKALOIDS.
-!- SUBUNIT: HOMOTETRAMER (PROBABLE).
-!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 svcdlssrsergelmntvanhf-h-gklnilvnnagiviykeakd-ytved-yslimsin 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 feaayhlsvlahpflk-asergnvvfissvsgalavpyeavygatkgamdqltrclafew 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 akdnirvngvgpgviatslvemtigdpegkenlnklidrcalrrmgepkelaamvaflcf 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 nlegctalvtg-gs-rgigygiveelasigas-vytcsrngkelndcltgwrskgfkvea 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 NLENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTY-RKERSRKE-LEKLLEQLNQPEA 60
                                  01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
TROPINONE REDUCTASE-II (EC 1.1.1.236) (TR-II)
DATURA STRAMONIUM (JIMSONNEED) (COMMON THORNAPPLE)
EUKARYOTA; PLANTA, EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1988 (REL. 06, CREATED)
01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
NODULATION PROTEIN G (HOST-SPECIFICITY OF NODULATION PROTEIN C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match
12.2%; Score 214; DB 9; Length 260;
Local Similarity 24.5%; Pred. No. 7.07e-15;
les 63; Conservative 82; Mismatches 97; Thank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NADP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29555C68 CRC32;
          260 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159 159 B
260 AA; 28311 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                            FAMILY (SDR).

EMBL; L20474; G424162; -.
OXIDOREDUCTASE; NADP.
NP_BIND 17

ACT_SITE 159 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 paasyvtgqiiyvdggl 254
      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               236 DLSSGVTGENIHVDSGF 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEBELLE F., SHARMA S.B.;
                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RHIZOBIUM MELILOTI.
PLASMID SYM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 87016382
TRN2_DATST
P50163;
                                                                                                                                                                                                                        TISSUE-ROOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NODG_RHIME
P06234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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STRAIN-HB101
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P25529;
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ACT_SITE
SEQUENCE
                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps 13;
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PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULIATIVELY ANAEROBIC RODS;
ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 PDNIRVNAISAGPIRTLSAKGVGGFNTILKE-IEERAPLKRNVDQVEVGKTAAYLLSDLS 238
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STRAIN=K12 / MG1655;
MEDLINE; 95334362.
MEDLINE; 95334362.
MEDRINE; 95334362.
BLATTNER F.R.;
NUCLEIC ACIDS RES. 23:2105-2119(1995).
FAMILY (SDR).
FAMILY (SDR).
EMBL; U14003; G537108; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 tamfrltreitg-qmirrrngriinvtsvagaignpgqtnycaskagmigfskslaqeia 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 trnitvncvapgfi-e-sam-tdklnhkqkekimvaipihrmgtgtevasavaylasdha 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55 klfpanlanrdevkalggraeadlegvdilvnnagitk-dglflhmadpdwd-ivlevnl 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 mfeltgrkalvtgasg--aiggaiarvlhagga-iv-glhgtgiek-letlatelgdr-v 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MINLENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYRKERSRKELEKLLEQLNQPEA 60
                                                                                                             FISHER R.F., SWANSON J.A., MULLIGAN J.T., LONG S.R.; GENETICS 117:191-201(1987).
-i- FUNCTION: PROPOSED TO MODIFY NOD FACTOR FAITY ACYL CHAIN.
-i- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 197; DB 6; Length 245;
Pred. No. 2.12e-12;
73; Mismatches 108; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
HYPOTHETICAL OXIDOREDUCTASE IN PEPA-GNTV INTERGENIC REGION
(FCC 1. - . - . ) (F254).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAD OR NADP (BY SIMILARITY).
BY SIMILARITY.
; 908F3A66 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 6; Length 245;
                                                                                                                                                                                                                                                                                                                                                     254 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ECOGENE; EG12540; YJGU.
PROGITE; PS00061; ADH_SHORT.
HYPOTHETICAL PROTEIN; OXIDOREDUCTASE.
ND RIND
37
NAD OR N
NUCLEIC ACIDS RES. 14:7453-7472(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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01-FEB-1995 (REL. 31, LAST SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27563 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.2%;
Local Similarity 24.1%;
nes 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             229 ayvtgqtihvnggmami 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       239 SGVTGENIHVDSGFHAI 255
                                                                                                                                                                                                                                          EMBL; (SDR).

EMBL; X04379; G46308; -.

EMBL; Y00604; G46304; -.

PIR; C24706; C24706.

PIR; S07675; S07675.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LT 14
YJGU_ECOLI
P39345;
                                                                                             STRAIN-1021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NP_BIND
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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   REPRESENTATION OF THE PROPERTY OF THE PROPERTY
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PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                           119 taví-lvsgavtrhmverkagkvinicsmgselgrdtitpyaaskgavkmltrgmcvela 177
                                                                                                                                                                                                                                                                                    120 ISSYSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVONYNVMGVAKASLEANVKYLALDLG 179
                                                                                                                                                                                                                                                                                                                            178 rhniqvngiapgyfktemtkalvedeaftawlckrtpaarwgdpqeligaavflsskasd 237
                                                                                                                                                                                                                                                                                                                                                      -:- SUBUNIT: HOMOTETRAMER.
-:- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
FAMILY (SDR).
EMBL; D10497; G216571; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YOSHIMOTO T., HIGASHI H., KANATANI A., LIN X.S., NAGAI H., OYAMA H., KURAZONO K., TSURU D.;
J. BACTERIOL. 173:2173-2179(1991).
                                                                                                            4 lfslagknilitg-sa-qgigfillatglgkygaqiiinditaeraelaveklhqegiqav 61
Score 183; DB 11; Length 254;
Pred. No. 2.07e-10;
76; Mismatches 114; Indels 7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1992 (REL. 22, CREATED)
1-MAY-1992 (REL. 24, LAST SUDGENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
7-ALPHA-HYDROXYSTEROID DEHYDROGENASE (EC 1.1.1.159) (7-ALPHA-HSDH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 179; DB 4; Length 255;
Pred. No. 7.54e-10;
74; Mismatches 101; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26778 MW; 443F6382 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      255 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ECOGENE; EG10425; HDHA.
PROSITE; PS00061; ADH_SHORT.
OXIDOREDUCTASE; NAD; BILE ACID CATABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 10.2%;
Best Local Similarity 25.7%;
Matches 65; Conservative
      Ouery Match
Best Local Similarity 21.8%;
                                                55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A38527; A38527.
PIR; JT0951; JT0951.
HSSP; P19992; 1HDC.
                                                                                                                                                                                                                                                                                                                                                                                                                   238 fvnghllfvdgg 249
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240 GVTGENIHVDSG 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 255 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 96264882
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在安全的人,是一个人,我们的人,我们的人的人,也是不是一个的,我们的人,我们的人,也是有一个人,也是我们的人,也是我们的人,我们的人,我们的人,我们的人,我们的人,		*************************************

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Dec 4 16:00:39 1997; MasPar time 8.20 Seconds 384.011 Million cell updates/sec Jular output not generated.

1 MINLENKTYVIMGIANKRSI..........LSSGVIGENIHVDSGFHAIK 256 >US-08-790-043A-1 (1-256) from US08790043A.pep 1753 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

Searched:

101610 seqs, 12294212 residues

Post-processing:

Minimum Match 0% Listing first 45 summaries

a-geneseq28
1.part1 2.part2 3.part3 4.part4 5.part5 6.part6 7.part7
8.part8 9.part9 10.part10 11.part11 12.part12 13.part13
14.part14 15.part15 16.part16 17.part17 18.part18
19.part19 20.part20 21.part21 Database:

Mean 33.197; Variance 180.878; scale 0.184 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	1 250-17	1000	6.84e-1/	6.84e-17	8.65e-16	8.65e-16	4.15e-14	4.15e-14	5.28e-04	8.41e - 04	2.09e-02	2.09e-02	9.35e-02	9.35e-02	9.35e-02	9.35e-02	1.69e-01	3.05e-01	3.53e-01	4.73e-01	10-000 1	10 000.
Description		Stearoy1-Acr-desacuta	M. smegmatis InhA.	M. smegmatis InhA.	M. tuberculosis inhA	M. tuberculosis InhA.	Mycobacterium bovis I	M. bovis InhA.	7-alpha-hydroxy stero	Gluconate: NADP+-5-oxi	Rape leaf beta-ketoac	Rape seed beta-ketoac	Acetoacetyl CoA reduc	Sequence encoded by t	Acetyl-CoA reductase.	Acetyl-CoA-reductase.	N-acetyl mannosamine	NAD affinity glucose	Glucose dehydrogenase	Acetoacetvl CoA reduc	Oleccondinate deprination	elucose denyulogenase
II	1 0 0	K23/93	R66293	R66289	R66290	R66901	R66292	863900	R22993	W02111	R89323	R89322	R10974	R32192	P94157	R71324	R14145	R27756	R27757	197770	10 C 0 C C	PBUU63
DB	;; .	4	12	12	12	15	15	1	7	20	15	15	2	œ	, ,	13	m	មា) LC		4	H
* Query Match Length		385	269	269	269	000	7 2 6	22.0	0 C	255	315	315	246	246	246	329	269	261	100	1 4 5	7	261
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۵	Sequence of glucose d	Acetoacetyl CoA reduc	5	M. bovis pS5 ORF1 pro	ucose dehydroge	Thermostable glucose		erus	Acetyl-CoA reductase.	Modified glucose dehy	Sequence of human alp	Alpha-1-antitrypsin m	Entire sequence of co	Alpha-1-antitrypsin m	times alpha-1-antitry	Human arpina r angrest	-I-antitrypsin	ragm	Sednence encoded by h	ŏ	trypsin	8	rphe3581 alphal-antit	a	5 6	9	[Gly358] alphal-antit	
	P80590	R10679	R66291	6889	R04044	5	P61477	R77866	551750		P40134	R67362	203754	D67363) (K6/300	m	R04033	P50877	P50021	R22931	W10220	D61713	1010	٠:	7	P61708	
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	261	241	247	247	261	1 1 2 0	1 0	24.0	273	261	412	394	100	* 000	* 0	394	394	399	418	418	418	256	200	100	3.94	394	394	
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ALIGNMENTS

T 1 R23793 standard; Protein; 385 AA. R23793;	04-NOV-1992 (first entry) Stearoyl-ACP-desaturase (from clone pDES7). Delta-9-desaturase; stearoyl-ACP; oleoyl-ACP; lipid; biosynthesis.	Brassica napus var. Rafel.	. Location/Qualifiers	otide 173	sig_pep	otein 74385	/label= mat_protein	NL9002130-A.	16-APR-1992.	28-SEP-1990; 002130.	-SEP-1990; NL-002130.	(TEWE-) STICHTING TECH WETENSCHAPPEN.	1; 92-157514/19.	N-PSDB; Q24482.	Cruciferous stearoyl-ACP-desaturase coding sequences	modifying lipid blosynthesis in plants, esp. ollseed rape	sclosure; Fig 2; 31pp; Dutch	Stearoyl-ACP-desaturase catalyses the conversion of stearoyl-ACP	into oleoyl-ACP. Vectors contg. the sequence encoding this entyme	have been used to transform petunia and oilseed rape plants using	robacterium tumefaciens, resulting in altered lipid blosynchesis	and modification of lipid composition of the plant.	quence 385 AA;	. Match 20.8%; Score 365; DB 4; Length 385;	cal Similarity 38.1%; 67; Conservative
T 1 R23793 sta: R23793;	04-NOV-199 Stearoyl-A Delta-9-de	Brassica n	Key	Peptide	/label= si	Protein	/label= ma	NL9002130-	16-APR-199	28-SEP-199	28-SEP-199	(TEWE-) SI	WPI; 92-15	N-PSDB; 02	Cruciferor	modifying	Disclosure	Stearoyl-	into oleo	have been	Agrobacte	and modif:	Sequence	erv Match	Best Local S Matches 6
RESULT ID R AC R	DT DE	so	FH	FT	FT	FT	FI	PN	PD	PF	PR	PA	DR	DR	ΡŢ	ΡŢ	PS	ပ္ပ	ပ္ပ	ပ္ပ	ပ္ပ	ပ္ပ	SO	Ö	M Be

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Ouery Match
Best Local Similarity 35.0%; Pred. No. 6.84e-17;
Matches 92; Conservative 60; Mismatches 92; Indels 19; Gaps 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 eldvqneehlstladritaeigegnkidgvvhaigfmpqsgmginpffdapyedvskgih 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ::||::| :: | ::| | |||| |:|:| | ::| | |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      isoniazid - useful in diagnosis, treatment and prevention of mycobacterial infection, e.g. tuberculosis.
Disclosure; Fig. 4A-4B; 104pp; English.
The gene from Mycobacterium smegnatis encoding InhA (R66293), the target of action for isoniazid, was identified, isolated, cloned and sequenced (Q75517). Mutant inhA genes have been used for recombinant vaccine development.
                                                             03-JUL-1995 (first entry)
M. smegmatis InhA.
Isonazid; isonicotinic acid hydrazide; INH; inhA gene; vaccine.
Mycobacterium smegmatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  De LISLE GW, Jacobs WR, Wilson IM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polynucleotide(s) determining mycobacterial resistance to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-JUL-1995 (first entry)
M. smegmatis Inha.
Isonazid; isonicotinic acid hydrazide; INH; inhA gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   BANERJEE A.
COLLINS D.
JACOBS W R.
UNIV YESHIVA EINSTEIN COLLEGE.
R66293 standard; Protein; 269 AA. R66293;
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R66289 standard; Protein; 269 AA.
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                                                                                                                                                                                                                                    24-NOV-1994, U05398.
13-MAY-1993, NZ-247620.
14-MAY-1993, US-062409.
31-MAR-1994; US-221742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (WILS/) WILSON T M.
Banerjee A. Collins D,
WPI; 95-006691/01.
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13-MAY-1993; NZ-247620.
14-MAY-1993; US-062409.
31-MAK-1994; US-221742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mycobacteria; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                      (AGRE-) AGRESEARCH.
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• 4

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Score 355; DB 12; Length 269;
Pred. No. 6.84e-17;
60; Mismatches 92; Indels 19; Gaps 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig. 4; 76pp; English. Mycobacterium tuberculosis and Genes from Mycobacterium smegmatis, Mycobacterium tuberculosis and Mycobacterium bovis that encode Inha, the target of action for isoniazid, were identified, isolated and cloned. Sequences of the 3 genes are given in Q78913-15, and encoded amino acids in R66289-91. Mutant genes have been used in recombinant vaccine
                                                                                                                                                                                                                                                                                                                                                   Gene target for isonicotinic acid hydrazide - used to develop prods for diagnosis, treatment, prevention and studies involving mycobacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M. tuberculosis inhA gene.
Isonazid; isonicotinic acid hydrazide; INH; inhA gene;
vaccine; mycobacteria; ds.
(BANE/) BANERJEE A.
(COLL/) COLLINS D M.
(COLLS) DE LISEE G W.
(JACO) JACOBS W R.
(WILS/) WILSON T M.
(WILS/) WILSON T M.
(COLL/) COLLINS D.
(ESSH ) UNIV YESHIYA BINSTEIN COLLEGE.
BANERJEE A. COllins DM, De LISLE GW, Jacobs WR;
WHY SOLD TM, COLLINS D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jacobs WR;
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(COLL/) COLLINS D M.
(JACO/) JACOBS W R.
(WILS/) WILSON T M.
(AGRE-) AGRESBARCH.
(COLL/) COLLINS D.
(YESH ) UNIV YESHIVA EINSTEIN COLLEGE.
Banerjee A. COllins DM, De LISLE GW, Jr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R66290 standard; Protein; 269 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 20.3%;
Local Similarity 35.0%;
les 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-JUL-1995 (first entry)
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12-MAY-1994; U05344.
13-MAY-1993; NZ-247620.
14-MAY-1993; US-062409.
31-MAR-1994; US-221742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Banerjee A, Collins
Wilson TM, Collins D;
                                                                                                                                                                                                                                                                                                 WPI; 95-006366/01.
N-PSDB; Q78913.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                          Score 340; DB 12; Length 269;
Pred. No. 8.65e-16;
68; Mismatches 92; Indels 19; Gaps 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 kygvrsnlvgagpirtlamsaivggalgeeagagiglleegwdgrapigwnmkdatpvak 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 isaygmdfdprallpimnpggsivgmdf-dpsrampaynwmtvaksalesvnrfvareag 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 ISSYSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLG 179
                                                                                                                                                                                                                                                                                                                                                                                                             62 eldvqneehlaslagrvteaigagnkldgvvhsigfmpqtgmginpffdapyadvskgih 121
                                                                                                                                                                                                                                                                                                                5 ldgkrilvsgiitdssiafhiarvaqeqgaqlvlt-gfdrlrl-iqritdrl-pakapll 61
                                                                                                                                                                                                                                                                                                                                                  4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYRKERSRKELEKLLEQLNQPEAHLY 63
                                                                              Disclosure: Fig. 4: 76pp; English.

Disclosure: Fig. 4: 76pp; English.

Genes from Mycobacterium smegmatis, Mycobacterium tuberculosis and Mycobacterium bovis that encode InhA, the target of action for Isoniazid, were identified, isolated and cloned. Sequences of the 3 genes are given in Q78913-15, and encoded amino acids in R66289-91. Mutant genes have been used in recombinant vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polynuclectide(s) determining mycobacterial resistance to isoniazid - useful in diagnosis, treatment and prevention of mycobacterial infection, e.g. tuberculosis.

Mycobacterial infection, e.g. tuberculosis.

Disclosure; Fig. 4; 104pp; English.

The gene from Mycobacterium tuberculosis encoding InhA (R66901), the target of action for isoniazid, was identified, isolated, cloned and sequenced (075518). Mutant inhA genes have been used for recombinant vaccine development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isonazid; isonicotinic acid hydrazide; INH; inhA gene; vaccine.
Mycobacterium tuberculosis.
                                           prods for diagnosis, treatment, prevention and studies involving mycobacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (YESH ) UNIV YESHIVA EINSTEIN COLLEGE. (WILS/) WILSON T M. Banerjee A, Collins D, De LISLE GW, Jacobs WR, Wilson TM; WPI; 95-006691/01.
                    N-roub; V/0914.
Gene target for isonicotinic acid hydrazide - used to develop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 340; DB 12;
Pred. No. 8.65e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 tvcallsdwlpattgdiiyadggaht 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    229 TAAYLLSDLSSGVTGENIHVDSGFHA 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T
R66901 standard; Protein; 269 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 19.4%;
Best Local Similarity 32.7%;
                                                                                                                                                                                                                                               19.4%;
Local Similarity 32.7%;
les 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-JUL-1995 (first entry)
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13-MAY-1993; NZ-247620.
14-MAY-1993; US-062409.
31-MAR-1994; US-221742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M. tuberculosis InhA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BANERJEE A. COLLINS D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGRE-) AGRESEARCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JACOBS W R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            269 AA;
                                                                                                                                                                                                                 269 AA;
WPI; 95-006366/01.
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                                                                                                                                                                                                   development.
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                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BANE/)
                                                                                                                                                                                                                                                         Query Match
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68; Mismatches 92; Indels 19; Gaps 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 ldgkrilvsgiltdssiafhlarvaqeggaglvlt-gfdrlrl-iqritdrl-pakapll 61
                                                                                                                                                                                                                              181 kygvrsnlvgagpirtlamsaivggalgeeagaqiqlleegwdqrapigwnmkdatpvak 240
                                                                                                                                                                                                                                               180 PDNIRVNAISAGPIRTLSAKG-VGG-F--NT---I--LKEI-EERAPLKRNV-DQVEVGK 228
                                                                                                                                                              122 isaygmdfdprallpimnpggsivgmdf-dpsrampaynwmtvaksalesvnrfvareag 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 317; DB 12; Length 231;
Pred. No. 4.15e-14;
53; Mismatches 77; Indels 9; Gaps
                                                                                                                64 QIDVQSDEEVINGFEQIGKDVG--N-IDGVYHSIAFANMEDL-RGRESETSREGFLLAQD 119
                                                                                                                                                                                   62 eldvqneehlaslagrvteaigagnkldgvvhsigfmpqtgmginpffdapyadvskgih 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probacterial infections may provide the major property of the property of action for incompanies of the property of action for incompanies of the property of action for incompanies was designated pS5. The sequence of pS5 was determined (Q78915), revealing 2 large open reading frames, ORF2 being the InhA gene encoding the protein given
                                                     5 ldgkrilvsgiitdssiafhiarvaqeqgaqlvlt-gfdrlr1-iqritdr1-pakapll 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene target for isonicotinic acid hydrazide - used to develop prods for diagnosis, treatment, prevention and studies involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isonazid; isonicotinic acid hydrazide; INH; InhA gene; pS5 gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jacobs WR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (YESH) UNIV YESHIVA EINSTEIN COLLEGE. Banerjee A, Collins DM, De LISLE GW, Wilson TM, Collins D;
                                                                                                                                                                                                                                                                                                   241 tvcallsdwlpattgdiiyadggaht 266
                                                                                                                                                                                                                                                                                                                              229 TAAYLLSDLSSGVTGENIHVDSGFHA 254
                                                                                                                                                                                                                                                                                                                                                                                     .T
R66292 standard; Protein; 231 AA.
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nes 66; Consermation
                                                                                                                                                                                                                                                                                                                                                                                                                                    03-JUL-1995 (first entry) Mycobacterium bovis InhA.
          87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-MAY-1993; NZ-247620.
14-MAY-1993; US-062409.
31-MAR-1994; US-221742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mycobacteria.
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(COLL) COLLINS D M.
(DLIS/) DE LISLE G W.
(JACO/) JACOBS W R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (WILS/) WILSON T M. (AGRE-) AGRESEARCH. (COLL/) COLLINS D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium bovis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-MAY-1994; U05344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-NOV-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vaccine;
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             Matches
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Location/Qualifiers

"unknown amino acid"

Misc_difference J04058883-A.

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122 isaysyasmakallpimnpggsivgmdf-dpsrampaynwmtvaksalesvnrfvareag 180
                       Isonazid; isonicotinic acid hydrazide; INH; inhA gene; pS5; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polynucleotide(s) determining mycobacterial resistance to isoniazid useful in diagnosis, treatment and prevention of bisoliazid useful in diagnosis, treatment and prevention of mycobacterial infection, e.g. tuberculosis.

A cosmid library of Mycobacterium bovis G4/100 was made in vector prUBIS and transferred into Mycobacterium snegmatis mc2155. The phenotype on M. snegmatis was designated pss. Sequencing of pss revealed 2 open reading frames. ORF2 encoded InhA (R61899), the target of action for isoniazid. Mutants of the inhA gene have been used for recombinant vaccine development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                De LISLE GW, Jacobs WR, Wilson TM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match
Local Similarity 32.2%; Pred. No. 4.15e-14;
les 66; Conservative 53; Mismatches 77. Thale
                                                                                                                                                                                                                                                                                                                                                                                                                                              UNIV YESHIVA EINSTEIN COLLEGE.
                                                                  181 kygvrsnlvaagpirtlamsamlgg 205
                                                                                    R63900 standard; Protein; 231 AA.
                                                                                                                                                                                                 03-JUL-1995 (first entry)
                                                                                                                                                                                                                                                                                              24-NOV-1594;
13-MAY-1994; UOS398.
13-MAY-1993; NZ-247620.
14-MAY-1993; US-062409.
31-MAR-1994; US-221742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (WILS/) WILSON T M.
Banerjee A, Collins D,
WPI; 95-006691/01.
                                                                                                                                                                                                                                                                                                                                                                                               BANERJEE A.
                                                                                                                                                                                                                                                                                                                                                                          AGRE-) AGRESEARCH
BANE/) BANERJEE A
                                                                                                                                                                                                                                                                                                                                                                                                                          JACOBS W R.
                                                                                                                                                                                                                                                                                                                                                                                                              COLLINS D.
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                                                                                                                                                                                                                        bovis InhA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; Q75519
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P. 22-JUN-1990; 165391.

P. 22-JUN-1990; JP-165391.

R. VIKA-) SHIN NIPPON KAGAKU.

R. WPI, 92-118055/15.

R. PSDB; 023902.

T. Alpha-hydroxy steroid dehydrogenase prepn. - by extracting enzyme from E. coil obtd. by transformation.

The gene for 7 alpha-hydroxy steroid dehydrogenase was introduced into a suitable plasmid and used to transform E. coil. The transformant can express a large amt. of the enzyme. The transformant is cultivated in culture medium at pH 7.0 at 37 deg. C. transformant is cultivated in culture medium at pH 7.0 at 37 deg. C. transformated with ammonium sulphate. The resuspended pellet was desalted and passed over an ion exchange column to recover purified sequence 255 AA; each be used as a biochemical reagent.

Score 174; DB 4; Length 255; Pred. No. 5.28e-04; 73; Mismatches 100; Indels 15; Gaps 13;

Match 9.9%; Local Similarity 26.0%; Les 66; Conservative

Query Match Best Loc Matches

g ŏ g ò d

δ

9; Gaps

53; Mismatches 77; Indels

atches

ò g ò g

7 lridgkcaiitg-aga-gigkeiaitfatxgasvvvsdinadaanhvvdeigqlg-ggaf 63

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NADP+-5-Oxido:reductase gene - esp. by increasing copy no. in Gluconobacter, used as intermediate for ascorbic and tartaric acids claim 8; Page 10-12; 15pp; German.

The gluconobacter oxydans gene may be used to transform cells, to produce higher levels of gluconate:NADp+-5-Oxidoreductase.

Tartaric acid can now be produced without the difficult Sequence 256 AA;
                                                                                                                                                                                                                                                                                                                                                   5-keto.gluconate prodn. by increasing expression of gluconate:
                                                                                                                                                                       Gluconate:NADP+-5-oxidoreductase.
Gluconate; NADP; oxidoreductase; Gluconobacter oxydans; ascorbic acid; tartaric acid; ds.
Gluconobacter oxydans.
                                                                                                                                                                                                                                                           07-FEB-1996; 101776.
07-FEB-1995; DE-003946.
(RHEI-) RHEIN BIOTECH GES NEUE BIOTECHNOLOGISCHE.
Bringer-Meyer S, Hollenberg CP, Klasen R, Sahm H;
                                                                                                                         W02111 standard; Protein; 256 AA.
                                                                                                                                                       06-MAR-1997 (first entry)
                                        236 aswvsgqiltvsgg 249
                                                                   238 SSGVTGENIHVDSG 251
                                                                                                                                                                                                                                                                                                                       WPI; 96-364397/37.
N-PSDB; T36145.
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                                                                                                             RESULT
ID WO
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                                                                                                                                                                    62 eldvqneehlaslagrvteaigagnkldgvvhaigfmpqtgmginpffdapyadvskg1h 121
                                                                                                                                                                                      122 isaysyasmakallpimnpggsivgmdf-dpsrampaynwmtvaksalesvnrfvareag 180
                                                                                                                                                                                                                                                5 ldgkrilvsgiitdssiafhiarvaqeggaqlvlt-gfdrlrl-1gritdrl-pakapll 61
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19-AuG-1992 (first entry)
7-alpha-hydroxy steroid dehydrogenase.
Biochamical reagent.
Escherichia coli.

R22993 standard; Protein; 255 AA

R22993;

181 kygvrsnlvaagpirtlamsamlgg 205 :| | ::|||||||: :: || 180 PDNIRVNAISAGPIRTLSAKGV-GG 203

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Query Match 8.6%; Score 150; DB 15; Length 315;
Best Local Similarity 23.4%; Pred. No. 2.09e-02;
Matches 58; Conservative 67; Mismatches 110; Indels 13; Gaps 13;
                                           Gaps 13;
                                                                                                                                                                                                                                                                                                                                                                                            132 -AKKLMPEG-GSIVATTYLGGEFAVONYNVMGVAKASLEANVKYLALDLGPDNIRVNAIS 189
                                                                                                                                                                                                                                                                                                                                                                    190 pgyfatemterlvad-eeftdwlckrtpagrwggveel-vg-aavflssrassfvnggvl 246
                                                                                                                                                                                                                                                                           130 varhmiprgrgkivnicsvqselarpgiapytatkgavknltkgmatdwgrhglqingla 189
                                                                                                                                                                                  74 avidgvaaierdmgpidilinnagiqrraplee-fsrkdwdd-lmstnvna-vf-fvgga 129
                                                                                                                                                                                                                           72 EVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDISSYSLTIVAHE 131
                                                                                      15 lvtgasrgigltlakglarygaevvlngrnaesldsaqsgfea-eglkastavfdvtdqd 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oilseed plant, e.g. for production of transgenic rape plants with low or modified oil content, diversion of metabolism to alternative storage compounds, e.g. starch, protein or engineered polymers, or production of plants with enhanced oil content. The DNA may also
                                                                                                                                    12 MGIANKRSIAFGVAKVLDQLGAKLVFTYRKERSRKELEKLLEQLNQPEAHLYQIDVQSDE 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated rape beta-ketoreductase DNA - used to develop plants with lower or higher oil contents or with altered oil compsn. Claim 2; page 16; 29pp; English.

The sequence corresponds to a rape leaf beta-ketoreductase encoded by a cDNA insert in plasmid pJRL6.2 in Escherichia coli XLI-Blue. A plastid stroma targeting transit peptide is present. DNA encoding the protein may be inserted in a vector or expression cassette in sense or antisense orientation for expression in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rape leaf beta-ketoacyl-ACP-ketoreductase.
Rape; leaf; beta-ketoacyl-ACP-ketoreductase; beta-ketoreductase; plasmid pJR16.2; cDNA library; Escherichia coli; vector; plastid; stroma; transit peptide; cassette; antisense; oilseed; transgenic plant; crop improvement; lipid; metabolic engineering; polymer; rapessed oil.

Brassica napus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 be used as a probe to obtain similar genes from other plants.
transit peptide may be used to direct other proteins to leaf
Score 171; DB 20; Length 256;
Pred. No. 8.41e-04;
74; Mismatches 100; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Elborough K, Fentem PA, Slabas AR, White A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R89323 standard; Protein; 315 AA.
  Query Match 9.8%;
Best Local Similarity 24.0%;
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-APR-1996 (first entry)
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17-JUL-1995; G01678.
20-JUL-1994; GB-014622.
(ZENE ) ZENECA LTD.
Chase D, Elborough K, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Transit peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            315 AA;
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N-PSDB; Q99305.
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74 vvvvtgasrgigkaialslgkagckvlvnyarsakeaeevskqieayg-gqaitfggdvs 132

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Query Match
8.6%; Score 150; DB 15; Length 315;
Best Local Similarity 23.4%; Pred. No. 2.09e-02;
Matches 58; Conservative 67; Mismatches 110; Indels 13; Gaps 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 vvvvtgasrgigkaialslgkagckvlvnyarsakeaeevskqieayg-gqaitfggdvs 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 VAHEAKKLMPE-GGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDNIRVN 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249 vvcpgfiasdmtak-lge-d-mekkilgtiplgrygqpedvaglveflalspaasyitgg 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 VIMGIANKRSIAFGVAKVLDQLGAKLVFTY-RKERSRKELEKLLEQLNQPEAHLYQIDVQ 68
                                                                                                                                                                           249 vvcpgflasdmtak-1ge-d-mekkilgtiplgryggpedvaglveflalspaasyitgg 305
                                                                                                                                                                                                     128 VAHEAKKIMPE-GGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDNIRVN 186
133 keadv-eammktaidawgtidvvvnnagitr-dtllirmkksgwde-vidlnltgvflct 189
                                      69 SDEEVINGFEQIGKDV-GNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDISSYSLTI 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oilseed plant, e.g. for production of transgenic rape plants with low or modified oil content, diversion of metabolism to alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated rape beta-ketoreductase DNA - used to develop plants with lower or higher oil contents or with altered oil compsn. Claim 1; Page 15; 29pp; English.

The sequence corresponds to a rape seed beta-ketoreductase encoded by a cDNA insert in plasmid pJRS10.1 in Escherichia coll XLI-Blue. A plastid stroma targeting transit peptide is present. DNA encoding the protein may be inserted in a vector or expression cassette in sense or antisense orientation for expression in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               storage compounds, e.g. starch, protein or engineered polymers, or production of plants with enhanced oil content. The DNA may also be used as a probe to obtain similar genes from other plants. The transit peptide may be used to direct other proteins to seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rape seed beta-ketoacyl-ACP-ketoreductase.
Rape, seed; beta-ketoacyl-ACP-ketoreductase; beta-ketoacyl-ACP-ketoreductase; beta-ketoacyl-ACP-ketoreductase; beta-ketoreductase; plasmid pJRS10.1; cDNa library; embryo; Escherichia coli; vector; plastid; stroma; transit peptide; cassette; antisense; oilseed; transgenic plant; crop improvement; lipid; metabolic engineering; polymer; rapesseed oil.
Brassica napus.
                                                                                     190 qa-atkimmkkrkgriiniasvvglignigqanyaaakagvigfsktaaregasrninvn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ZENE ) ZENECA LTD.
Chase D. Elborough K, Fentem PA, Slabas AR, White A;
WPI; 96-105914/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                             T 11
R89322 standard; Protein; 315 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-APR-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Transit peptide"
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17-JUL-1995; G01678
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66 dstktafdkvksevgevdvlinnagitrdvvfr-kmtradwda-vidtnlts--lfnvtk 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 EAKKLMPE-G-GSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDNIRVNAI 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 spgylatdmvkairq-d-vldkivatipvkrlglpeeiasicawlsseesgfstgadfsl 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189 SACPIRTLSAKGVGGFNTILKEIEERAPLKRNVDQVEVGKTAAYLLSDLSSGVTGENIHV 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-1993 (first entry)
Sequence encoded by the acetoacetyl-CoA reductase (phbB) gene of the polyhydroxybutyrate (PHB) operon
Operon; polyhydroxyalkanoate; acetoacetyl-CoA reductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Gaps
                                                                                                                                                                                                   Polyester biopolymers; polyhydroxybutyrate; polyhydroxy alkanoate; beta ketothiolase; acetoacetyl CoA reductase.
                                                                                                                                                                                                                                                                                                                                                                   Construction and modification of polyester bio:polymers - by introduction of poly-hydroxy-butyrate and -alkanoate genes into bacteria or plants.

This Alcaligenes eutrophus acetyl CoA reductase is an enzyme which is essential to the biosynthesis of polyhydroxyalkanoate (PHA). The gene encoding this is contained in plasmid clone, pAeT3, downstream from the thiolase gene. The use of recombinant methods for producing such enzymes, required for polyester blosynthesis process.

Synthesis process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 246;
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B.0%; Score 140; DB 2; Length 246;
Local Similarity 22.2%; Pred. No. 9.35e-02;
hes 41; Conservative 59; Mismatches 77; Indels
                                                                                                                                    R10974 standard; Protein; 246 AA.
                                                                                                                                                                                      Acetoacetyl CoA reductase enzyme
                                                                                                                                                                                                                                                                                                            (MASI ) MASSACHUSETTS INST TECH.
Peoples OP, Sinskey AJ;
WPI; 91-051441/07.
N-PSDB; Q10501.
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13-JUL-1992; U05786.
19-JUL-1991; US-732243.
(UYMA-) UNIV MADISON JAMES.
(UNMS) UNIV MICHIGAN STATE.
                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                              10-JUL-1990; U03851.
10-JUL-1989; US-378155.
                                                                                                                                                                                                                                 Alcaligenes eutrophus. W09100917-A.
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                                             306 aftidggi 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                246 AA;
                                                                           245 NIHVDSGF 252
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Transgenic plants producing poly:hydroxy-alkanoate polymer(s) -
Transgenic plants producing poly:hydroxy-alkanoate polymer(s) -
Transgenic plants and PHA synthase

Transgenic plants and PHA synthase

Disclosure; F10 2; 70pp; English.

The nucleotide sequence of the PHB operon was obtained from Janes, B.

Hollar, J. and Dennis, D. in Dawes, E.A. (ed.) Novel Biodegradable

Polymers, Kluwer Academic Publishers, 175-190 (1990). It contains

the genes from PHB synthase, 3-ketothiolase and acetoacetyl-CoA

reductase. The inventors claim a transgenic plant material contg;

foreign DNA encoding a peptide which exhibits 3-ketothilase activity,

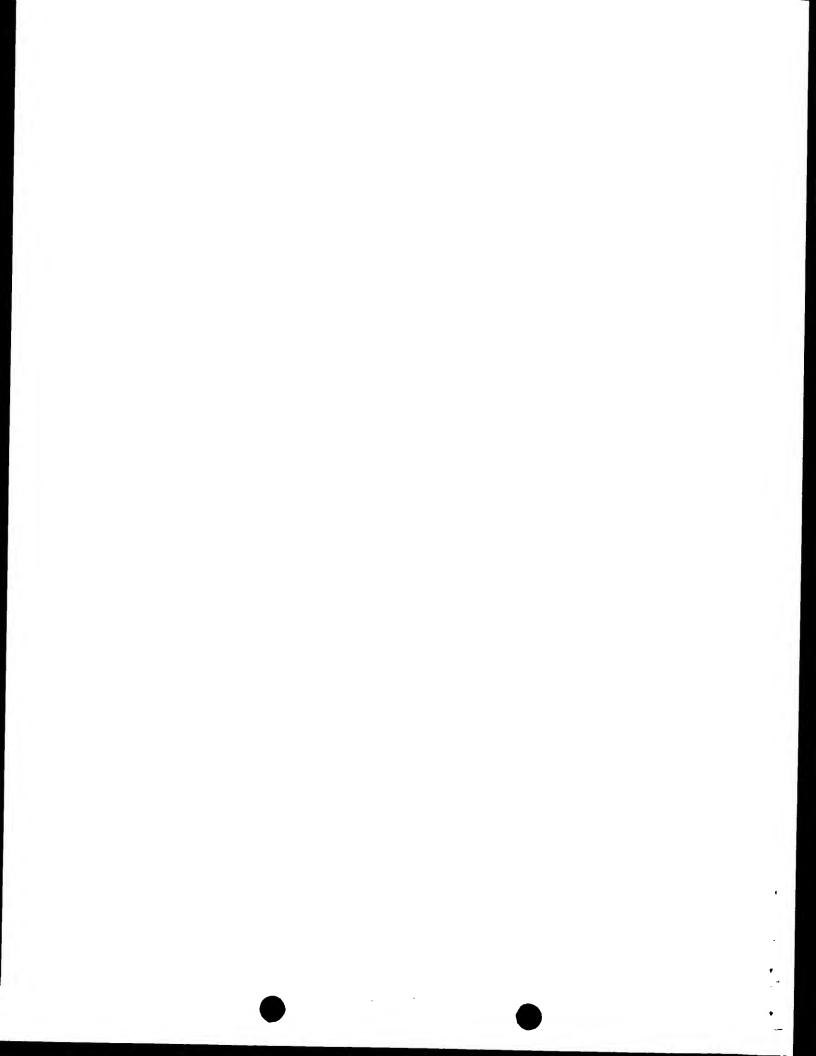
foreign DNA agene), 842-2611 (Phb C gene) or 3952-4692 (Phb B

Sequence 246 AA;
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The enzyme is used to study the polyhydroxybutyrate (PHB) biosynthetic pathway. It catalyses the reduction of acetoacetyl CoA to form D(·)·beta-hydroxybutyryl-coA, the substrate for PHB synthetase, and can be used to control biopolymer syntheses and produce new biopolymers. See also P94154-P94156.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 dstktafdkvksevgevdvlinnagitrdvvfr-kmtradwda-vidtnlts--lfnvtk 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 spgylatdmvkairg-d-vldkivatipvkrlglpeelasicawlsseesgfstgadfsl 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polyester biopolymers; acetyl-CoA reductase; polyhydroxybutyrate; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.0%; Score 140; DB 6; Length 246; Larity 22.2%; Pred. No. 9.35e-02; Conservative 59; Mismatches 77; Indels
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Pred. No. 9.35e-02;
59; Mismatches 77; Indels
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Poirier Y, Somerville CR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P94157 standard; protein; 246 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alcaligenes eutrophus H16
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les 41; Conservative
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27-JUN-1988; U02227.
29-JUN-1987; US-067695.
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WPI; 89-039655/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 2
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                             WPI; 93-058785/07.
N-PSDB; Q36660.
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12-JUN-1990
Dennis DE,
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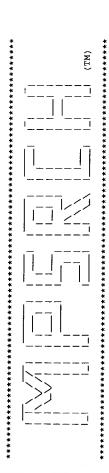
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205 qvidgmadrgwgrivnissvngqkgqfgqtnystakaglhgftmalaqevatkgvtvntv 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ransgenic plant material with plastid(s) contg. the enzymes for Transgenic plant material with plastid(s) - express synthesis of poly:hydroxy:alkanoate(s) - express poly:hydroxy:butyrate and have good growth and seed formation. Claim 2: Page 60-61: 88pp; English.

The acetyl-CoA-reductase gene (phbB) from A. eutrophus is cloned under the control of an Arabidopsis thalians seed storage protein promoter for plastid tissue-specific gene expression in a promoter for plastid tissue-specific gene expression in a transgenic plant. When expressed with the 3-ketchholase (phbA) and poly-beta-hydroxyalkanoate-synthase (phbC) genes, a chiange protein play-beta-hydroxyalkanoate (PhA), specifically poly-beta-for hydroxyalkanoate (PhA), specifically poly-beta-for hydroxyalkanoate (PhB), is expressed in the transgenic plant (preferably a Brassica e.g. rape). PHB and related PHAs are biodegradable thermoplastics with many useful applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149 dstktafdkvksevgevdvlinnagitrdvvfr-kmtradwda-vidtnlts--lfnvtk 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ery Match
st Local Similarity 22.2%; Pred. No. 9.35e-02;
tches 41; Conservative 59; Mismatches 77; Indels 8; Gaps
182 spgyiatdmvkairg-d-vldkivatipvkrlglpeeiasicawlsseesgfstgadfsl 239
                                                                                              Acetyl-CoA-reductase.
Acetyl-CoA-reductase. transgenic plant;
poly-beta-hydroxyalkancate; poly-beta-hydroxybutyrate;
blodegradable thermoplastic.
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R71324 standard; Protein; 329 AA.
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17-AGG-1993; US-108193.
06-JUN-1994; US-254357.
(UNMS ) UNIV MICHIGAN STATE.
                                                                                                                                                                                                                                                                                                            21-OCT-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                         Alcaligenes eutrophus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; Q85642
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Fri Dec



Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

: uo

Thu Dec 4 16:10:30 1997; MasPar time 4.09 Seconds 307.588 Million cell updates/sec sular output not generated.

>US-08-790-043A-1 (1-256) from US08790043A.pep 1753 1 MALENKTYVIMGIANKRSI......LSSGVTGENIHVDSGFHAIK 256 Description: Perfect Score: Scoring table: Sequence:

55487 segs, 4918616 residues PAM 150 Gap 11 Searched:

Minimum Match 0% Listing first 45 summaries Post-processing: Database:

a-issued 1:backl 2:51 3:52 4:53 5:54 6:55 7:56 8:PCT90 9:PCT91 10:PCT92 11:PCT93 12:PCT94 13:PCT95 14:PCT96

Mean 29.990; Variance 162.121; scale 0.185 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

th DB ID Description Pred. No. 15229279-7 Patent No. 55229279-7 Patent No. 55229279-7 Patent No. 55229279-7 1306-02 73 1 5512669-4 Patent No. 5512669-7 2.156+00 18 1 5512669-4 Patent No. 5512669-7 2.156+00 18 1 05-08-121-8 Sequence 3, Applicatio 6.796+00 64 13 PCT-US95-1 Sequence 4, Applicatio 6.796+00 64 7 US-08-375- Sequence 2, Applicatio 6.796+00 99 7 US-08-002- Sequence 2, Applicatio 6.796+00 94 7 US-08-002- Sequence 6, Applicatio 7.826+00 94 7 US-08-002- Sequence 6, Applicatio 7.826+00 94 7 US-08-002- Sequence 6, Applicatio 2.406+01 01 11 PCT-US93-1 Sequence 5, Applicatio 2.406+01 01 18 CM-08-089-1 Sequence 5, Applicatio 2.406+01 01 01 02-08-08-08-08-08-08-08-08-08-08-08-08-08-	8 Applicatio 2
Description 5229279-7 Patent No. 5 5512669-4 Patent No. 5 5512669-4 Patent No. 5 5512669-4 Patent No. 5 572669-4 Patent No. 5 572669-4 Patent No. 5 67269-7 Performed 3, 105-08-121- Sequence 3, 105-08-121- Sequence 1, 105-08-121- Sequence 6, 105-08-121- Sequence 6, 105-08-121- Sequence 51, 105-07-121- Sequence 52, 105-08-121- Sequence 2, 105-08-121- Sequenc	ω,
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RESULT

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                                                                                                                                                                                                                                                                                                 Score 108; DB 1; Length 273;
Pred. No. 2.15e+00;
29; Mismatches 50; Indels 3; Gaps
                                                                                          APPLICANT: PEOPLES, OLIVER P.; SINSKEY, ANTHONY J.
TITLE OF INVENTION: GENE ENCODING BACTERIAL ACETOACETYL-COA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 5512669
APPLICANT: PEOPLES, OLIVER P.; SINSKEY, ANTHONY J.
TITLE OF INVENTION: GENE ENCODING BACTERIAL ACETOACETYL-COA
                                                                                                                                                                                                                                                                                                                                                                                    219 AIP--EKVLNERIIPQIPVGRLGEPDEIARIVVFLASDEAGFITGSTISANGG 269
                                                                                                                                                                                                                                                                                                                                                                                               200 GVGGFNTILKE-IEERAPLKRNVDQVEVGKTAAYLLSDLSSGVTGENIHVDSG 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.2%; Score 108; DB 1; Length 273;
                                                                                                                     NUMBER OF SEQUENCES: 7
CURRENT APPLICATION DATA:
FILING DATE: 29-ANG-1994
PRIOR APPLICATION DATE: 129-ANG-1993
APPLICATION NUMBER: 124,570
FILING DATE: 20-SEP-1993
APPLICATION NUMBER: 944,488
FILING DATE: 03-NOV-1922
APPLICATION NUMBER: 566,535
FILING DATE: 13-ANG-1990
APPLICATION NUMBER: 66,535
FILING DATE: 13-ANG-1990
APPLICATION NUMBER: 67,695
FILING DATE: 29-JUN-1987
 296 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/297,667
FILING DATE: 29-AUG-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                              296 AA; 31345 MW; 472090 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              296 AA; 31345 MW; 472090 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 124,570
FILING DATE: 20-SEP-1993
APPLICATION NUMBER: 944,488
FILING DATE: 03-NOV-1992
APPLICATION NUMBER: 566,535
FILING DATE: 13-AGC-1190
APPLICATION NUMBER: 67,695
FILING DATE: 29-JUN-1987
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 PRT;
                                                                                                                                                                                                                                                                                                    Query Match 6.2%;
Best Local Similarity 27.4%;
Matches 31; Conservative
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 STANDARD;
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                                                            Patent No. 5512669.
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                                                                                 Patent No. 5512669
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                                                                                                                                                                                                                                                            SEQ ID NO:4:
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                                       01-JAN-1900
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ID 5512669-4
XX AC XXXXXX
5512669-4
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Sequence 3, Application PC/TUS9308322
GENERAL INFORMATION:
APPLICANT: Sager, Ruth
TITLE OF INVENTION: MASPIN, A NOVEL SERPIN WITH TUMOR SUPPRESSING ACT
                                                                      159 GRIVNISSINGQKGQMGQANYSAAKAGDLGFTKALAQEGAAKGITVNAICPGYIGTEMVR 218
                                                                                                                    140 GSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDNIRVNAISAGPIRTLSAK 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 100; DB 11; Length 418;
Pred. No. 6.79e+00;
21; Mismatches 30; Indels 2; Gaps
                                                                                                                                                                    219 AIP--EKVLNERIIPQIPVGRLGEPDEIARIVVFLASDEAGFITGSTISANGG 269
                                                                                                                                                                                             200 GVGGFNTILKE-IEERAPLKRNVDQVEVGKTAAYLLSDLSSGVTGENIHVDSG 251
Pred. No. 2.15e+00;
29; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                  418 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 558X
OPERATING SYSTEM: MS-DOS (Version 5.0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 00530/072001
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/938,823
FILING DATE: 09/01/92
APPLICATION NUMBER: 07/844,296
FILING DATE: 02/28/92
APPLICATION NUMBER: 07/662,216
FILING DATE: 02/28/31
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
SEQUENCE 418 AA; 46736 MW; 945384 CN;
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REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 0053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                               STANDARD;
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Best Local Similarity 27.4%;
Matches 31; Conservative
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Best Local Similarity 25.4%;
Matches 18; Conservative
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02110-2804
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CITY: Boston
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PCT-US93-08322-3
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RESULT 6
ID PCT-US95-16930-4
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Pred. No. 6.79e+00;
21; Mismatches 30; Indels 2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08121714
Patent No. 5470970
GENERAL INFORMATION:
APPLICANT: Sager, Ruth
TITLE OF INVENTION: MASPIN, A NOVEL SERPIN WITH
TITLE OF INVENTION: TÜMOR SUPPRESSING ACTIVITY
NÜMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                         STATE: Massachusetts
COUNTRY: U.S.A.
2IP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 553X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/121,714
                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/938,823
FILING DATE: 09/01/92
APPLICATION NUMBER: 07/844,296
FILING DATE: 02/28/92
APPLICATION NUMBER: 07/662,216
FILING DATE: 02/28/92
APPLICATION NUMBER: 07/662,216
FILING DATE: 02/28/91
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 34,819
REGISTRATION NUMBER: 34,819
REGISTRATION NUMBER: 34,819
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-8906
TELEPHONE: (617) 542-8906
                                                           418 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
CE 418 AA; 46736 MW; 945384 CN;
                                                           PRT;
                                                                                                                 Sequence 3, Application US/08121714.
                                                                                                                                                                                                              E: Fish & Richardson
225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                            STANDARD;
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Best Local Similarity 25.4%;
Matches 18; Conservative
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87 IDGVYHSIAFA 97
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CITY: Boston
     158 VKKLYHSEAFT 168
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               : :||| ||:
87 IDGVYHSIAFA 97
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US-08-121-714-3
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307 LIKVLGGLYSYRRDFVIRCIDQVLENIERGLE-INDYGQNMHRISNVRYLTEIFN-FEMI 364
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9
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Pred. No. 6.79e+00;
25; Mismatches 30; Indels
                                                                                                                                                                                                                         APPLICANT: UNIVERSITY OF MASSACHUSETTS MEDICAL SCHOOL TITLE OF INVENTION: HETEROLOGOUS POLYPEPTIDE TITLE OF INVENTION: PRODUCTION IN THE ABSENCE OF TITLE OF INVENTION: NONSENSE-MEDIATED MRNA DECAY TITLE OF INVENTION: FUNCTION NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUW TYPE: FORM:

MEDIUW TYPE: FORM:

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATCHIN PC-DOS/MS-DOS

SOFTWARE: PATCHIN PATA:

APPLICATION NUMBER: PCT/US95/16930
FILING DATE: 27-DEC-1995
FRICH APPLICATION NUMBER: US 08/375,300
FILING DATE: 20-DEC-1995

ATTORNEY/AGENT INFORMATION:

NAME: FASSE, J. PETCT

REGISTRATION NUMBER: 32,983

REFERENCE/DOCKET NUMBER: 32,983

REFERENCE/DOCKET NUMBER: 32,983

REFERENCE/DOCKET NUMBER: 04020/046W01

TELEFRAX: (617)542-8906

TELEFRAX: (617)542-8906

TELEFRAX: (617)542-8906

TELEFRAX: CO1154

INPORMATION FOR EXO ID NO: 4:
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764 AA
                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street Suite 3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
SEQUENCE 764 AA; 89464 MW; 2913896 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
PRT;
                                                                                                                                                                                  Sequence 4, Application PC/TUS9516930 GENERAL INFORMATION:
                                                                                                                                        Sequence 4, Application PC/TUS9516930.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGIH: 764 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 29.1%;
Matches 25; Conservative
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CORRESPONDENCE ADDRESS:
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                                            APPLICANT: Feng, He
APPLICANT: Jacobson, Allan S.
TITLE OF INVENTION: HETEROLOGOUS POLYPEPTIDE PRODUCTION IN
TITLE OF INVENTION: THE ABSENCE OF NONSENSE-MEDIATED MRNA DECAY FUNCT
                                                                                                                                                                                                                                                                                                                                                                                                                                307 LIKVLGGLYSYRRDFVIRCIDQVLENIERGLE-INDYGQNMHRISNVRYLTEIFN-FEMI 364
                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                            Query Match 5.7%; Score 100; DB 7; Length 764; Best Local Similarity 29.1%; Pred. No. 6.79e+00; Matches 25; Conservative 25; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application PC/TUS9516930
GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF MASSACHUSETTS MEDICAL SCHOOL
TITLE OF INVENTION: HETEROLOGOUS POLYPEPTIDE
TITLE OF INVENTION: PRODUCTION IN THE ABSENCE OF
TITLE OF INVENTION: FUNCTION FUNCTION
NUMBER OF SEQUENCES: 6
                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/375,300
FILING DATE: 20-JAN-1995
ATTOREY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1089 AA
                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street Suite 3100
                                                                                                                                                                                                                                                                     04020/046001
                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein FINCE 764 AA; 89464 MM; 2913896 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application PC/TUS9516930.
                    Sequence 4, Application US/08375300
Patent No. 5679566
GENERAL INFORMATION:
                                                                                                                                                                                                                                             NAME: Fease, J. P.
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET UNMBER: 0402(
TELECOMMUNICATION: TELEPHONE: (617)542-8906
TELER: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
 Sequence 4, Application US/08375300.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     365 KSDV-LLDTIYHIIRFGHINNQPNPF 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                764 amino acids
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                                                                                                                                                                                                                                                                                                                                                    single
                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                               Boston
                                                                                                                                                  USA
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                                                                                                                                                 COUNTRY:
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RESULT
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Sequence 2, Application US/08375300
Patent No. 5679566
GENERAL INFORMATION:
APPLICANT: Peng, He
APPLICANT: Jacobson, Allan S.
TITLE OF INVENTION: HETEROLOGOUS POLYPEPTIDE PRODUCTION IN
TITLE OF INVENTION: THE ABSENCE OF NONSENSE-MEDIATED MENA DECAY FUNCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                       COUNTY: USA

COUNTY: USA

COUNTY: USA

COMPUTER READBALE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM FC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/16930

FILING DATE: 27-DEC-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/375,300

FILING DATE: C3-JAN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Fasse, J. Peter

REGISTRATION NUMBER: 32,983

REFERENCE/COCKET NUMBER: 04020/046WO1

TELEPPAX: (617)542-5070

TELEPPAX: (617)542-8906

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE: CHARACTERISTICS:

LENGTH: 1089 anito acide
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Best Local Similarity 29.1%; Pred. No. 6.79e+00;
Matches 25; Conservative 25; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1089 AA.
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street Suite 3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street Suite 3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
JENCE 1089 AA; 126746 MW; 5973553 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 GKDVGNIDGVYHSIAFANMEDLRGRF 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1089 amino acids
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ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDALL
STREET: ZZL
                                        Boston
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                                                              STATE:
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US-08-790-043A-1.rai

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                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Thomas, Garry
APPLICANT: Anderson, Eric D
APPLICANT: Thomas, Laurel
APPLICANT: Thomas, Laurel
APPLICANT: Hayfilsk, Joel S
TITLE OF INVENTION: Methods and Reagents for Inhibiting
TITLE OF INVENTION: Furin Endoprotease
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti and Witcoff, Ltd.
                                                                                                                                                                                                                                                              / Match 5.7%; Score 100; DB 7; Length 1089; Local Similarity 29.1%; Pred. No. 6.79e+00; les 25; Conservative 25; Mismatches 30; Indels (
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/375,300
FILING DATE: 20-JAN-1995
ATTORNEY/AGENT INFORMATION:
RAME: FESSE, J. P.
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 32,983
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFHONE: (617)542-5070
TELEFAX: (617)542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/002,202
FILING DATE: 08-JAN-1993
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Allegretti and Witcoff, Ltd.
10 South Wacker Drive, Suite 3000
                                                                                                                                                                                                                             MOLECULE TYPE: protein
SEQUENCE 1089 AA; 126746 MW; 5973553 CN;
                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/08002202
Patent No. 5604201
GENERAL INFORMATION:
                                                                                                                                   TELERAX: (617)cr.
TELERAX: 200154
INFORMATION FOR SEQ. ID NO: 2: SEQUENCE CHARACTERISTICS:
FONGTH: 1089 amino acids
                                                                                                                                                                                                                                                                                                                                          Db ' 690 KSDV-LLDTIYHIIRFGHINNQPNPF 714
                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/08002202
                                                                                                                                                                                                             not relevant
                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 10 South
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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FEATURE:
NAME/KEY: Protein
LOCATION: 1..334
COTHER INFORMATION: /label= Variant
OTHER INFORMATION: /note= "This amino acid sequence is the amino ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: sequence of the modified alpha-1-antitrypsin OTHER INFORMATION: protein, alpha-1-antitrypsin Portland;" ICE 394 AA; 44432 MM; 838791 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 ILEGLNFNLT-EIPEAQIHEGFQELLRTLNQPDSQL-QLTTGNGLFLSQGLKLVDKFLED 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11, Application US/08002202
Patent No. 5604201
GENERAL INFORMATION:
APPLICANT: Thomas, Garry
APPLICANT: Thomas, Laurel
APPLICANT: Thomas, Laurel
APPLICANT: Hayflick, Joel S
TITLE OF INVENTION: Methods and Reagents for Inhibiting
TITLE OF INVENTION: Furin Endoprotease
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 Match 5.6%; Score 99; DB 7; Length 394; Local Similarity 25.4%; Pred. No. 7.82e+00; nes 18; Conservative 20; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/002,202
FILING DATE: 08-JAN-1993
ATTORNEY APACTATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    394 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Allegretti and Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTR: USA
ZIP: 60606
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5604201nan, Kevin E
REGISTRATION NUMBER: 95,30003
REFERENCE/DOCKET NUMBER: 92,448
TELECOMOUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1000
TELEFAX: 312-715-1001
TELEFAX: 910-221-3317
INFOREMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/08002202.
                                                                                                                                                                                                                               LENGTH: 394 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                 linear
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US-08-002-202-11
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LENGIH: 647 amino acids
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                                                                                                                                                        /label= Variants
/note= "This amino acid sequence is the amino ac
                                                                                                                                                                                    OTHER INFORMATION: sequence of the modified alpha-1-antitrypsin OTHER INFORMATION: variant, alpha-1-antitrypsin Pittsburgh "ACE 394 AA; 44347 MW; 838436 CN;
                                                                                                                                                                                                                                                                   76 ILEGLNFNLT-EIPEAQIHEGFQELLRTLNQPDSQL-QLTTGNGLFLSQGLKLVDKFLED 133
                                                                                                                                                                                                                                                                               2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/08002202
Patent No. 5604201
GENERAL INFORMATION:
APPLICANT: Thomas, Garry
APPLICANT: Thomas, Laurel
APPLICANT: Hayflick, Joel S
TITLE OF INVENTION: Methods and Reagents for Inhibiting
TITLE OF INVENTION: Furin Endoprotease
                                                                                                                                                                                                                           Query Match 5.6%; Score 99; DB 7; Length 394; Best Local Similarity 25.4%; Pred. No. 7.82e+00; Matches 18; Conservative 20; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSE: Allegretti and Witcoff, Ltd.
ADDRESSE: Allegretti and Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: 111inois
COUNTRY: USA
NAME: NO. 5604201nan, Kevin E
REGISTRATION NUMBER: 35,30003
REFERENCE/DOCKET NUMBER: 92,448
TELECOMMUNICATION INFORMATION:
TELEPRAN: 312-715-1000
TELEPRA: 312-715-1234
TELER: 910-221-5317
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/002,202 FILING DATE: 08-JAN-1993 CLASSIFICATION: 514 ATTORNEY/AGENT INFORMATION: NO. 5604201nan, Kevin E
                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08002202.
                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 394 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                       NAME/KEY: Protein
LOCATION: 1..394
OTHER INFORMATION: ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                          Db - 134 VKKLYHSEAFT 144
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87 IDGVYHSIAFA 97
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US-08-002-202-6
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76 ILEGLNFNLT-EIPEAQIHEGFQELLRTLNQPDSQL-QLTTGNGLFLSQGLKLVDKFLED 133
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
CAPPLICATION NUMBER: US/08/218,943
FILLIG DATE: 28-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Schmaljohn, Connie S.
APPLICANT: ACCIain, David J.
APPLICANT: Dalrymple, Joel
APPLICANT: Dalrymple, Lonnie
TITLE OF INVENTION: HANTAVIRUS VACCINE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            647 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 71007/118/USGO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 28-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/799,479
FILING DATE: 14-NOV-1991
ATTOREY AGENT INFORMATION:
NAME: BENT, SLEEPHEN A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 394 AA; 44322 MW; 842374 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08218943 Patent No. 5614193 GENERAL INFORMATION:
REGISTRATION NUMBER: 35,30003
REFERENCE/DOCKET NUMBER: 92,4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-21-5317
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 394 amino acids
TYPE: amino acid
      35,30003
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy o
                                                                                                                                                                                                                                                                                                        Query Match 5.6%;
Best Local Similarity 25.4%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 VKKLYHSEAFT 144
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US-08-218-943-1
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RESULT
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                                                                                             249 VGNSAPIYVPTLDDFRSMEAFTGIFRSPHGEDHDLAGEEIASYS--IVGPANAK-VPHSA 305
                                                                                                         7; Gaps
                                                                                                                                                                                                                                                                                                                                            D4 Gene and Methods of Use Thereof
                                                       Score 97; DB 7; Length 647;
Pred. No. 1.04e+01;
23; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,945
                                                                                                                                                                                                                                                                                                                                                                        S: Kilpatrick & Cody
1100 Peachtree Street, Suite 2800
                                                                                                                                                                                             201 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROR APPLICATION: 435
PROR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNDRER: US 07/990,337
FILING DATE: December 10, 1992
ATTORNEY AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MEDIO7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 815-6508
          STRANDEDNESS: single
TOPOLOGY: linear
MULECULE TYPE: protein
MOLECULE ATAPP 72413 WW, 2325170 CN;
                                                                                                                                     306 S-SDTLSLIAYSGIPSYSSLSILTSSTEAK 334
                                                                                                                                                 Sequence 6, Application US/08292945
Patent No. 5585478
GENERAL INFORMATION:
APPLICANT: Lim, Bing
APPLICANT: Lim, Bing
APPLICANT: Adra, Chaker
APPLICANT: Ro, Jone
TITLE OF INVENTION: D4 Gene and Me
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                     Sequence 6, Application US/08292945.
                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (404) 815-6555
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 201 amino acids
amino acid
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Georgia
COUNTRY: United States
ZIP: 30309-4530
                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                         Query Match
Best Local Similarity 28.9%;
Matches 26; Conservative
  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                           CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
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US-08-292-945-6
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                                       SEQUENCE
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                                                                                                                                                                                                                                                                       73 LVCDSAPGPITMDLTGDLEALKKDTFVLKEGIE-YRVKINFKVNKDIVS-GLKYVQHTYR 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29 DQLGAKLVFTYRKERSRKELEKLLEQLNQPEAHLYQIDVQSDEEVINGFEQIGKDVGNID 88
                                                                                                                                                            15 DDLDSKLNYKPPPQKSLKELQEM-DKDDESLTK-YKKTLLGDVPVVADPTVPNVTVTRLS 72
                                                                                                                                                                                         4; Gaps
                                                                                                                        4; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US93/12074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.2%; Score 91; DB 11; Length 201; Best Local Similarity 23.0%; Pred. No. 2.40e+01; Matches 28; Conservative 27; Mismatches 63; Indels
                                                                              Query Match 5.2%; Score 91; DB 6; Length 201; Best Local Similarity 23.0%; Pred. No. 2.40e+01; Matches 28; Conservative 27; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201 AA
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APPLICATION NUMBER: US 07/990,337
FILING DATE: 10-DEC-1992
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 maino acids
IYPE: amino acid
STRANDEDNESS: single
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HCE 201 AA; 22979 MW; 226152 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                    ORGANISM: Murine
VCE 201 AA; 22979 MW; 226152 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: D4 Gene and NUMBER OF SEQUENCES: 8
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSIEM: PC-DOS/MS-DX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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ORIGINAL SOURCE:
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ORIGINAL SOURCE:
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PCT-US93-12074-6
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                                          SEQUENCE
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| 149 GG 150 οy

Search completed: Thu Dec 4 16:11:18 1997 Job time: 48 secs.

US-08-790-043A-1.rpr

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Thu Dec 4 16:01:38 1997; MasPar time 12.50 Seconds 591.864 Million cell updates/sec bular output not generated. uo u

>US-08-790-043A-1 (1-256) from US08790043A.pep 1753 1 MINLENKTYVIMGIANKRSI......LSSGVTGENIHVDSGFHAIK 256 Description: Perfect Score: Sequence: Title:

PAM 150 Gap 11 Scoring table:

91006 seqs, 28888923 residues Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

Database:

pir51
1:annl 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3 8:unann4 9:unann5 10:unann6 11:unann7 12:unann8 13:unann9 14:unann10 15:unenc 16:unrev

Mean 47.222; Variance 135.383; scale 0.349 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

4		æ			SOLVENING		
Alt No.	Score	Query	Query Match Length	A.C.	Ę	Docorring	70
				1		Description	
1	748	42.7	262	σ	\$48029	short-chain alcohol	2.41e-84
7	732	41.8	262	6	B43729	envM protein - Salmo	4.58e-82
m	718	41.0	295	σ	B64139	310	4.496-80
4	365	20.8	382	16	S17761	enoyl-acyl carrier p	4.05e-31
2	229		249	Ŋ	B37762		1.30e-13
9	224	12.8	244	S	JN0703	carbonyl reductase (5.31e-13
7	225	12.8	249	2	A31841	27K-2 protein (choli	4.01e-13
œ	219	12.5		Ŋ	A28053	adipocyte p27 protei	2.15e-12
σ	214	12.2		11	B48674	redu	8.66e-12
10	212	12.1		Ŋ	A28212	27K bile acid 7-dehy	1.51e-11
11	197	11.2		Н	C24706		9.25e-10
12	190	10.8	266	Ŋ	A42468	7alpha-hydroxysteroi	6.14e-09
13	183	10.4	254	σ	S56492	hypothetical protein	3.99e-08
14	182	10.4	254	σ	S34724	probable oxidoreduct	5.20e-08
15	181	10.3	262	16	A48950	aflatoxin biosynthes	6.78e-08
16	179		255	Ŋ	A38527	7alpha-hydroxysteroi	1.15e-07
17	171	9.6	256	ω	A57149	qluconate 5-dehydrog	9.38e-07
18	171	9.6	320	Ŋ	S22450	3-oxoacyl-[acyl-carr	9.38e-07
19	169	9.6	242	디	S39508	hypothetical protein	1.58e-06
20	169	9.6	261	σ	S56475	hypothetical protein	1.58e-06
21	168	9.6	268	11	C48674	tropinone reductase	2.04e-06

656 656 656 656 656 656 656 656	4.13e-04 2.28e-03 2.28e-03 2.90e-03 3.68e-03 7.54e-03
ט טפר או אט פועט	hypothetical protein acetoacetyl-CoA redu probable dehydrogena granaticin-producing glucose dehydrogenas hypothetical protein glucose 1-dehydrogen N-acylmannosamine 1-
X 00 L U U U U U U U U U U U U U U U U U	539737 RDALAE S25286 S05398 I39853 S35196 I40224 A43744
2446 2446 2446 11 2444 1444 144 1444 1444 1444 1444 1444 1444 1444 1444 1444 1444 1444 1444 144	7 7 7
vvvvvvvvvvvvvvvvvvv vvvv4vvvvvvvvvvvvv	
00000000000000000000000000000000000000	1441 1440 1333 1334 135
24476789991284896	20044444 20042845

ALIGNMENTS	RESULT 1 S48029 #type complete TITLE short-chain alcohol dehydrogenase homolog envM - Escherichia	ALTERNATE_NAMES enoy1-ACP reductase ORGANISM #formal_name Escherichia coli DATE 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 27-Oct-1995 ACCESSIONS 848030, 847681	Ŋ	IT S	##ccession 540K2 ##status preliminary ##molecule_type DNA ##residues 1.262 ##label KAT ##cross-references EMBL:X78733 REFERENCE A47681	#authors Bergler, H.; Hogenauer, G.; Turnowsky, F. #journal J. Gen. Microbiol. (1992) 138:2093-2100 #title Sequences of the envW gene and of two mutated alleles in #cross-references MUID:93123967 #accession A47681 preliminary	##molecule_type DNA ##residues 1-262 ##label BER ##cross-references NCBIN:121825; NCBIP:121826 ##note sequence extracted from NCBI backbone ##note #length 262 #molecular-weight 27864 #checksum 2286	Query Match 42.7%; Score 748; DB 9; Length 262; Best Local Similarity 44.4%; Pred. No. 2.41e-84; Matches 111; Conservative 65; Mismatches 71; Indels 3; Gaps 3;	Db 4 lsgkrilvtgvasklsiaygiagamhregaelaftyqndklkgrvæefaaqlg-sdivl- 61	Db 62 qcdvaedasidtmfaelgkvwpkfdgfvhsigfapgdqldqdyvnavtregfkiahdiss 121
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A64000
Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.;
Kirkness, E.F.; Kerlavage, A.R.; Bult, C.J.; Tonb, J.F.;
Dougherty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.;
FitzHugh, W.; Fleids, C.; Gocayne, J.D.; Scott, J.;
Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.F.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton,
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J. Bacteriol. (1989) 171:6555-6565
envM genes of Salmonella typhimurium and Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 sysfvamakacrtmlnpgsalltlsylgaeraipnynvmglakasleanvrymanamgpe 180
                                                                                                                                                     62 pcdvaedasidamfaelg-nvwpkfdgfvhsigfapgdqldgdyvnavtregfkvahdis 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 QIDVQSDEEVINGFEQIGKDV-GNIDGVYHSIAFANMEDLRGRFSET-SREGFLLAQDIS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 gvrvnaisagpirtlaasgikdfrkmlahceavtpirrtvtiedvgnsaaflcsdlsagi 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 YSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDN 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 SYSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPD 181
64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSET-SREGFLLAQDISS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B64139 *type complete
short chain alcohol dehydrogenase homolog (envW) homolog
Haemophilus influenzae (strain Rd KW20)
*formal_name Haemophilus influenzae
18-Aug-1995 *sequence_revision 18-Aug-1995 *text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYRKERSRKELEKLLEQLNQPEAHLY 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 lsgkrilvtgvasklsiaygiagamhregaelaftygndklkgrveefaaglgssiv-l- 61
                                                                                                                                                                                                                                                                                                                                                                           envM protein - Salmonella typhimurium
#formal_name Salmonella typhimurium
03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Gaps
                                                                                                                                 182 vrvnaisagpirtlaasgikdfrkmlahceavtpirrtvtiedvgnsaaflcsdlsagis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##cross-references GB:M31806
##cross-references GB:M31806
Y #hoross-references GB:M31806
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                                                                                                                                                                                                                                                                                                                                                              #type complete
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242 TGENIHVDSGF 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##molecule_type DNA
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                                                                                                                                                                                                                                                                  243 GENIHVDSGF 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##residues
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#title
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M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek, D.M.; Braandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.; Gnebm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C. Science (1995) 269:496-512
Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
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#title cDNA toloning and expression of Brassica napus enoyl-acyl carrier protein reductase in Escherichia coli.
#cross-references MUID:92003699
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#formal_name Brassica napus #common_name rape
22-Nov-1993 #sequence_revision 22-Nov-1993 #text_change
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Pred. No. 4.05e-31;
54; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                      9; Length 295;
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Pred. No. 4.49e-80;
70; Mismatches 69; Indels
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#length 385 #molecular-weight 40486
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Best Local Similarity 38.1%;
Matches 67; Conservative
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Best Local Similarity 43.2%;
Matches 108; Conservative
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tetrameric carbonyl reductase
#formal_name Sus scrofa domestica #common_name domestic pig
30-sep-1993 #sequence_revision 20-Aug-1994 #text_change
                                                                                                                                                                                                                                                            #journal J. Bacteriol. (1990) 172:4426-4426
#title Multiple copies of a bile acid-inducible gene in Eubacterium sp. strain VPI 12708.
                                                                                                                                                                                                                              Gopal-Srivastava, R.; Mallonee, D.H.; White, W.B.; Hylemon,
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blie acid 7-dehydroxylase - Bubacterium sp.
#formal_name Bubacterium sp.
a.1-May-1991 #sequence_revision 31-May-1991 #text_change
 #label SADH
#length 249 #molecular-weight 26658 #checksum 9638
                                                                                                                                                                                                                                                                                                                                                                                                                                      #authors Coleman, J.P.; White, W.B.; Hylemon, P.B.
#journal J. Bacteriol. (1987) 169:1516-1521
#title Molecular cloning of bile acid 7-dehydroxylase from Eubacterium sp. strain VPI 12708.
#cross-references MUID:87165759
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NCE A26938
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##molecule_type protein
##residues 1.22;123-136;138-151;166-175;187-201;240-244 ##label NA2
##residues is an NADPH-linked oxidoreductase that catalyzes the
T This enzyme is an NADPH-linked coxidoreductase that catalyzes the
reduction of various carbonyl compounds to the corresponding
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#journal J. Bacteriol. (1990) 172:7011-7019
#fitle cloning and sequencing of a bile acid-inducible operon from Eubacterium sp. strain VPI 12708.
#cross-references MUID:91072253
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Evidence for a multigene family involved in bile acid
7-dehydroxylation in Eubacterium sp. strain VPI 12708.
                                                    Biochem. Biophys. Res. Commun. (1993) 194:1311-1316 Cloning and sequence analysis of a CDNA encoding tetrameric carbonyl reductase of pig lung.
Nakanishi, M.; Deyashiki, Y.; Nakayama, T.; Sato, K.; Hara,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 KLMPE-G--GSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDNIRVNAISA 190
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31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change
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27K-2 protein (cholic acid-induced) - Bubacterium sp.
DaiA2 27K protein
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#length 244 #molecular-weight 25986 #checksum 8918
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12.8%; Score 224; DB 5; Length 244;
Best Local Similarity 24.2%; Pred. No. 5.31e-13;
Matches 44; Conservative 56; Mismatches 78; Indels
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                                                                                                                                                                                                        -244 ##label NAK
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240 gy 241 |: 251 GF 252

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y Match
12.8%: Score 225; DB 5; Length 249;
Local Similarity 23.7%; Pred. No. 4.01e-13;
hes 61; Conservative 81; Mismatches 103; Indels 12; Gaps 12;
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J. Cell Biol. (1988) 107:279-286
A growth factor-repressible gene associated with protein
kinase C-mediated inhibition of adipocyte differentiation.
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                                                                                                                                                                                                                                                                                                       116 nvtgvfngawcayqcmk-dakkgviintasvtgifgslsgvgypaskasviglthglgre 174
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#formal_name Mus musculus #common_name house mouse
19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change
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FICATION #superfamily ribitol dehydrogenase; short-chain alcohol
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                                                                            #label SADH
#length 249 #molecular-weight 26538 #checksum 8274
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                       dehydrogenase homology
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#accession S03382
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Best Local Similarity '
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#authors Coleman, J.P.; White, W.B.; Lijewski, M.; Hylemon, P.B.
#journal J. Bacteriol. (1988) 170:2070-2077
#title Nucleotide sequence and requiation of a gene involved in bile acid 7-dehydroxylation by Eubacterium sp. strain VPI 12708.
                                                                                                                                                                                        Nakajima, K.; Hashimoto, T.; Yamada, Y.
Proc. Natl. Acad. Sci. U.S.A. (1993) 90:9591-9595
Two tropinone reductases with different stereospecificities are short-chain dehydrogenases evolved from a common
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                                                                                                       03-May-1994 #sequence_revision 03-May-1994 #text_change
                                             tropinone reductase (EC 1.1.236) II - jimsonweed
#formal_name Datura stramonium #common_name jimsonweed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##experimental_source strain VPI 12708
FICATION #superfamily ribitol dehydrogenase; short-chain alcohol
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                                                                                                                                                                                                                                                                                                                                                                                                                              #length 260 #molecular-weight 28311 #checksum 3973
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12.2%; Score 214; DB 11; Length 260;
Local Similarity 24.5%; Pred. No. 8.66e-12;
hes 63; Conservative 82; Mismatches 97; Indels 15;
                             #type complete
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                                                                                   common thornapple
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#title
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                                                                                                                                              ACCESSIONS
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root hair infection and nodulation

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##experimental_source strain AK631 (a variant of strain 41)
the sequence reported in this reference is incorrect due
to multiple frameshift errors
T This is one of several proteins that control host specificity of
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Organization, structure and symbiotic function of Rhizobium
mellioti nodulation genes determining host specificity for
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I.; Gyoergypal, Z.; Barabas, I.; Wieneke, U.; Schell, J.;
Kondorosi, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fisher, R.F.; Swanson, J.A.; Mulligan, J.T.; Long, S.R. Genetics (1987) 117:191-201
Extended region of nodulation genes in Rhizobium meliloti 1021. II. Nucleotide sequence, transcription start sites and protein products.
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                                                                                                                                                   hsnC protein
#formal_name Rhizobium meliloti
30-Jun-1988_#sequence_revision 13-Jan-1995 #text_change
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#journal Nucleic Acids Res. (1986) 14:7453-7472
#title Nucleotide sequence of Rhizobium meliloti RCR2011 genes involved in host specificity of nodulation.
#accession C24706
                                                                                                                                                                                                                                                                                                                                                                                                                           175 iirknirvvgvapgvvdtdmtkglpp-e-iledylktlpmkrmlkpeeianvylflasdl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nodulation protein nodG - Rhizobium meliloti plasmid
                          #checksum 341
                                                             Score 212; DB 5; Length 249;
Pred. No. 1.51e-11;
80; Mismatches 106; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##residues 1-245 ##label DEB
##experimental_source strain RCR2011 symbiotic plasmid
NCE S06395
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##experimental_source strain 1021 symbiotic plasmid
                       #molecular-weight 26747
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#label SADH
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                                                             Query Match 12.1%;
Best Local Similarity 23.0%;
Matches 59; Conservative
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                   #length 249
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Score 197; DB 1; Length 245;
Pred. No. 9.25e-10;
73; Mismatches 108; Indels 14; Gaps 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #journal J. Bacteriol. (1991) 173:4558-4569
#title Cloning, sequencing, and expression of the gene coding for bile acid 7alpha-hydroxysteroid dehydrogenase from Eubacterium spp. strain VPI 12708.
                                                                                                                                                                                                                                                                                                                                                                                                55 klfpanlanrdevkalggraeadlegvdilvnnagitk-dglflhmadpdwd-ivlevnl 112
                                                                                                                                                                                                                                                                                                                                                                                                                          113 tamfrltreitq-qmirrrngriinvtsvagaignpgqtnycaskagmigfskslaqeia 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 SS-YSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 trnitvncvapgfi-e-sam-tdklnhkqkekimvaipihrmgtgtevasavaylasdha 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 PDNIRVNAISAGPIRTLSAKGVGGFNTILKE-IEERAPLKRNVDQVEVGKTAAYLLSDLS 238
                                                                                                                                                                                                                                                                                                                                       1 mfeltgrkalvtgasg--aiggalarvlhagga-iv-glhgtqiek-letlatelgdr-v 54
                                       plasmid
#superfamily ribitol dehydrogenase; short-chain alcohol
dehydrogenase homology
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7alpha-hydroxysteroid dehydrogenase (EC 1.1.1.159) -
Eubacterium sp. (strain VPI 12708)
#formal_name Eubacterium sp.
#formal_l992 #sequence_revision 18-Sep-1992 #text_change
23-Mar-1992
                                                                                                                                          #domain short-chain alcohol dehydrogenase homology
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#superfamily ribitol dehydrogenase; short-chain alcohol
                                                                                                                                                                                      #length 245 #molecular-weight 26088 #checksum 6343
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J. Biol. Chem. (1990) 265:9842-9849
Purification and characterization of a microbial,
NADP-dependent bile acid 7alpha-hydroxysteroid
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##cross-references GB:M58743
                                                                                                                                                                    #label SADH
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Best Local Similarity 24.1%;
Matches 62; Conservative
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239 SGVTGENIHVDSGFHAI 255
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Blattner, F.R.
Nucleic Acids Res. (1995) 23:2105-2119
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                                                                                                                                                                                                                                                                                                                                                  183 navlpg-mtatdavq-dnltddfrnfflkhtpiqrmglpeeiaaavvyfasddaayttgg 240
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                                                                                                                                                                                                                                                                                                     65 keetyvtmieeiiegegridvlvnnfgssnpkkdl-g-iantdpevfiktvninlksvfi 122
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                                                                            Score 190; DB 5; Length 266;
Pred. No. 6.14e-09;
72; Mismatches 102; Indels 11; Gaps
                                                                                                                                                                               10 VIMGIANKRSIAFGVAKVLDQLGAKLVFTYRK-ERSRKELEKLLEQLNQPEAHLYQIDVQ 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Gaps
                                                                                                                                                 7 vilvtastrgiglaiaqacakegakvymgarnlerakaradem-naaggnvkyvyn-dat 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein 1254 - Escherichia coli
#formal_name Escherichia coli
28-0ct-1995 #sequence_revision 03-Nov-1995 #text_change
03-Nov-1995
                 #domain short-chain alcohol dehydrogenase homology
                                 #label SADH
#length 266 #molecular-weight 28543 #checksum 3689
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Local Similarity 21.8%; Pred. No. 3.99e-08;
nes 55; Conservative 76; Mismatches 114; Indels
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Best Local Similarity 25.4%;
Matches 63; Conservative
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Viejo, M.; Enfedaque, J.; Regue, M. submitted to the EMBL Data Library, July 1993 Bacteriocin 28b from Serratia marcescens does not present lysis nor immunity genes downstream of the structural gene.
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#journal Appl. Environ. Microbiol. (1992) 581357-7837
#title Isolation characterization of a gene from Aspergillus parasiticus associated with the conversion of versicolorin A to sterigmatocystin in aflatoxin biosynthesis.
#cross-references MUD:93128930
#contents NRRL 5862
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#formal_name Aspergillus parasiticus
19-Dec-1993 #sequence_revision 19-Dec-1993 #text_change
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                                                                                                             834724 #type complete
probable oxidoreductase Serratia marcescens
#formal_name Serratia marcescens
13-Jan-1995_#sequence_revision 13-Jan-1995 #text_change
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##note sequence extracted from NCBI backbone

k# hote #length 262 #molecular-weight 28368 #checksum 9318
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Y #length 254 #molecular-weight 26613 #checksum 4302
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Pred. No. 5.20e-08;
70; Mismatches 111; Indels 15;
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##nolecule_type nucleic acid
##residues 1-262 ##label SKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1-254 ##label VIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##molecule_type DNA
##residne
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Best Local Similarity 24.3%;
Matches 63; Conservative
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240 GVTGENIHVDSG 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                        534724
                                                                                                                                                                                                                                                                                                                                                                                     #description
                                                                                                                                                                                                                                                                                                                                                      #submission
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REFERENCE
                                                                                       14
                                                                                                                                                                                                                                                                                                                           authors
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Length 262;

DB 16;

Score 181;

10.3%;

Best Local Similarity 26.9%; Pred. No. 6.78e-08; Matches 71; Conservative 74; Mismatches 97; Indels 22; Gaps 20;

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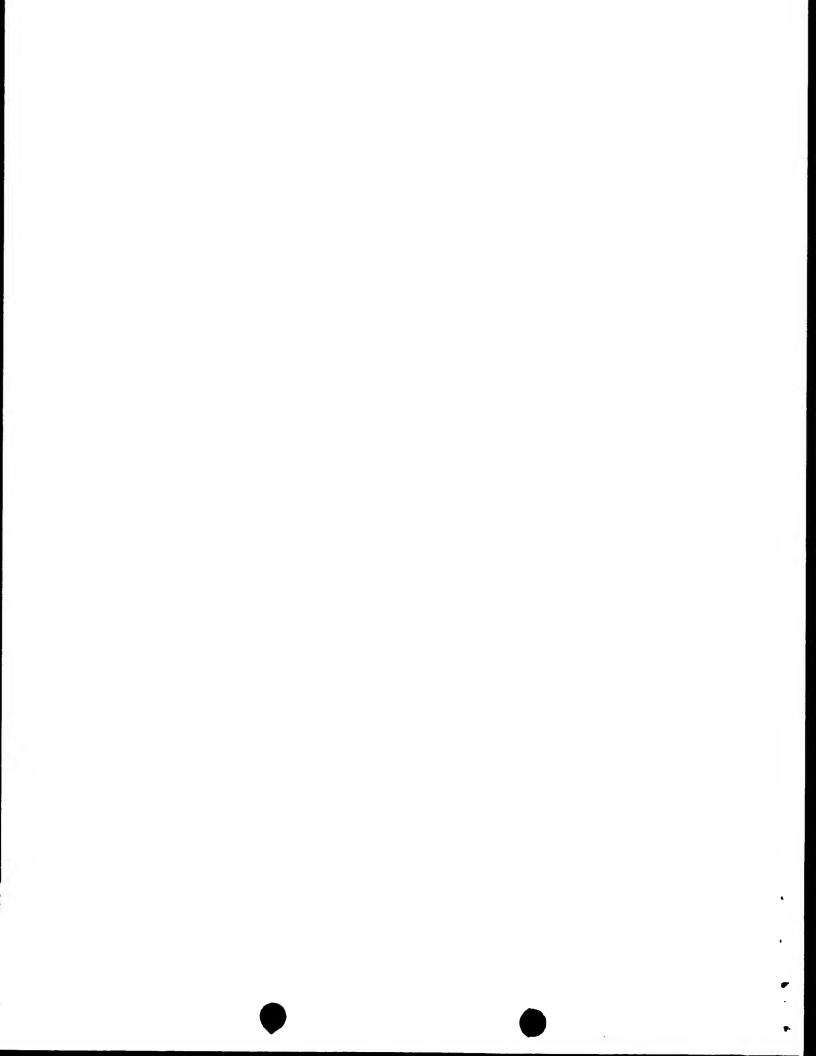
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239 sflasdtaewvsgkiigvdggafr 262 ::| || : |:| || :| 13 231 AYLLSDLSSGVTGENIHVDSG-FH 253

Search completed: Thu Dec 4 16:03:14 1997 Job time : 96 secs.



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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

on: Fri Dec 5 08:13:12 1997; MasPar time 44.49 Seconds 759.327 Million cell updates/sec

Title: >US-08-790-043A-2
Description: (1-771) from USO8790043A.seq
Perfect Score: 771
I ATGTTABATCTTGABABACAA........GATTCCACGCAATTABATAA 771
N.A. Sequence: TACAATTTAGAACTTTTGTT.........CTABAGGTGCGTTAATTATT
Comp:

Scoring table: TABLE default Gap 6

Gap 6 Nmatch STD: Dbase 0; Query 0 Searched: 82499 seqs, 21907491 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries Database: n-issued 1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:PCT90 9:PCT91 10:PCT92 11:PCT93 12:PCT94 13:PCT95 14:PCT96 Statistics: Mean 8.114; Variance 4.451; scale 1.823

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

			æ,					
Result No.	ult No.	Score	Query	Query Match Length	BB :	ar ar	Description	Pred. No.
Ų	-	55	7.1	7218	7	US-08-232-	Sequence 14, Applicati	4.32e-22
	7	27	3.5	215	9	US-08-238-	Sequence 5, Applicatio	4.14e-04
	m	27	3.5	242	7	US-08-273-	Sequence 1, Applicatio	4.14e-04
	4	24	3.1	215	9	US-08-238-	Sequence 5, Applicatio	2.03e - 02
	Ŋ	22	2.9	2894	7	US-08-483-	Sequence 1, Applicatio	2.43e-01
. (1)	φ	22	2.9	2894	7	US-08-472-	Sequence 1, Applicatio	2.43e-01
(1)	7	22	2.9	2894	9	US-08-278-	Sequence 1, Applicatio	2.43e-01
	ω	21	2.7	74	13	PCT-US95-1	Sequence 100, Applicat	8.12e - 01
C 1	σ	21	2.7	74	13	PCT-US95-1		8.12e-01
	10	21	2.7	81	13	PCT-US95-1	Sequence 98, Applicati	8.12e-01
e)	11	21	2.7	81	13	PCT-US95-1	Sequence 92, Applicati	8.12e-01
C	12	21	2.7	242	7	US-08-273-	Sequence 1, Applicatio	8.12e-01
	13	21	2.7	774	σ	PCT-US91-0	Sequence 1, Applicatio	8.12e-01
,	14	21	2.7	824	7	US-08-158-	Sequence 1, Applicatio	8.12e-01
U	15	20	2.6	75	13	PCT-US95-1	Sequence 99, Applicati	2.63e+00
່ດ	16	20	2.6	81	13	PCT-US95-1	Sequence 98, Applicati	2.63e+00
	17	20	2.6	82	13	PCT-US95-1	Sequence 97, Applicati	2.63e+00
	18	20	2.6	579	14	PCT-US96-0	Sequence 1664, Applica	2.63e+00
c	19	20	5.6	1265	7	US-08-182-	Sequence 5, Applicatio	2.63e+00

			2.63e+00	2.63e+00	2.63e+00	2.63e+00	2.63e+00	2.63e+00	8.26e+00					•		8.26e+00	8.26e+00	8.26e+00	8.26e+00	8.26e+00	•		8.26e+00	7	8.26e+00
Sequence 36, Applicati	Patent No. 5518915.	Patent No. 5171685.	Patent No. 5518916.	Patent No. 5177307.	No.517	ce 28,	Sequence 14, Applicati	1, Ap	14	93,	143,	94, 2	100	7,	٦,	1	Ļ	25,	1,	7	15,	37,	99	11,	Sequence 7, Applicatio
S-08-307-	518916-5		518916-5	177307-1	_	CT-US93-0			•	PCT-US95-1	US-08-471-				PCT-US91-0	PCT-US91-0	us-07-809-	PCT-US92-0	PCI-US92-0	PCT-US92-0	US-08-484-	PCT-US95-0	PCT-US95-0	US-07-718-	PCT-US96-0
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5.6	5.6	5.6	5.6	2.6	9	9.2	2.6	2.6	2.5	2.5	5	2.5	2.5	2.5	2.5	2.5	2.5	2.5	2.5	2.5	2	2	, C	2 . 2	2.5
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ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: BENNETT, Alan
APPLICANT: Abanvinch, John M.
APPLICANT: FOWELL, Ann
APPLICANT: STOTZ, Henrik
TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL
                                                                                                                                                               | | : :: :: ::: ::: ::: ::: ::: :::: | 701 AAYAAGTCAAGCGCTGTTTTACCTTGTTTTACTTGTTCATCTTGATCAAGGTGCA 642
                                                                                                                                                                                                                                                                                   521 AAATATTTAACATTTGCTTCGCTTTTAGCAACACCCATCACATTATAATTTTGA 462
                                                                                                                                                                                                                                                                                                                                                                                                                                       461 ACTGCGAATTGGCCAGCTAAATATGTTGTTGGAACAATGCTACCAGCTTCTGGCATTAAT 402
                                                                                                                                                 Gaps
                                                                                                                                               ö
                                                                          CLONE: pTZgpt-F1s
Sequence 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 other;
                                                                                                               Query Match 7.1%; Score 55; DB 7; Length 7218; Best Local Similarity 1.9%; Pred. No. 4.32e-22; Matches 7; Conservative 206; Mismatches 158; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LT 2
US-08-238-163-5 STANDARD; DNA; UNC; 215 BP.
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FILING DATE: 03-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/08238163
Sequence 5, Application US/08238163
Patent No. 5569830
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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                                                               IMMEDIATE SOURCE:
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                                                     TOPOLOGY:
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43 VCDTDTTYRVNNDSGHNKYSSANYNYGGNNVGAAKTHYYTHTNVSGADSKTVTDSYNASG 102
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                                                                                                                                                                                                                                                                                                                                                 428 TIGCAACAACATAITIAGGIGGGAAIICGCAGTICAAAAITAIAAIGIGAIGGGIGIIG 487
                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 1.215
OTHER INFORMATION: /standard_name= "Deduced amino acid
OTHER INFORMATION: sequence of PGIP from bean."
Sequence 215 BP: 15 A: 8 C: 25 G: 26 T: 141 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SCHREIBER, ALAN D.
APPLICANT: PARK, JONG-GU
TITLE OF INVENTION: METHODS OF STIMULATING PHAGOCYTOSIS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                               Ouery Match 3.5%; Score 27; DB 6; Length 215; Best Local Similarity 17.8%; Pred. No. 4.14e-04; Matches 26; Conservative 55; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.

CONPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHITIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,846
         ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 2307E-540
TELEPHONE: (415) 543-9600
TELEPHONE: (415) 543-5603
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 base pairs
TYPE: nucleic acid
STREE in uncleic acid
STREE in uncleic acid
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US-08-273-846-1 STANDARD; RNA; UNC; 290 BP.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08273846. Sequence 1, Application US/08273846 Patent No. 5641863 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    161 AKNSADGKVGSKNNGDRNNRYGTGTK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                    : |: ::|:: |:: |||:
488 CTAAAGCGAGCTTAGAAGCAAATGTT 513
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                                                                                                                                                       single
                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                  unknown
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                 TOPOLOGY:
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01-JAN-1900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Gaps 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :|::|| :: || :: || | : || |: || 368 ACTCATTAACAATTGATGAGGTGGTAGCATTG 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: /standard_name= "Deduced amino acid
OTHER INFORMATION: sequence of PGIP from bean."
Sequence 215 BP; 15 A; 8 C; 25 G; 26 T; 141 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 3.5%; Score 27; DB 6; Length 242;
Local Similarity 17.8%; Pred. No. 4.14e-04;
nes 26; Conservative 55; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,163
                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) Sequence 290 BP; 17 A; 34 C; 8 G; 11 T; 220 other;
                                                                                                                                                                                                                                                                                                                                                         US-08-238-163-5 STANDARD; DNA; UNC; 215 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-MAY-1994 (NI: 800 TXN: 800 
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                                                                                                                                                                                                                                                     Insufficient memory to reconstruct alignment.
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/08238163.
Sequence 5, Application US/08238163.
Sequence 5, Application US/08238163.
Patent No. 5569830
GENERAL INFORMATION.
APPLICANT: BENNETT, Alan
APPLICANT: LABAVITCH, John M.
APPLICANT: POWELL, Ann
APPLICANT: STOTZ, Henrik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCORNEY AGENT INFORMATION:
NAME: BASTIAN, KEVIN L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 2307E
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TELEFAX: (703) 816-4100 INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS:
                                                                                LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 03
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                            XXXXXX
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     88888888888
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PLANT INHIBITORS OF FUNGAL
POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL
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103 TSSSNGGTDGN-RSG-ADSYGSSKTAMTSRNRTGKTANNAVDSRNMGDASVGSDKNTKKH 160
                           58 HNKYSSANYNYGGANVVGAAKTHYYTHTNVSGADSKTVTDSYNASGTSSSNGGTDGNRSGA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 1.215
OTHER INFORMATION: /Standard_name= "Deduced amino acid
OTHER INFORMATION: sequence of PGIP from bean."
Sequence 215 BP; 15 A; 8 C; 25 G; 26 T; 141 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 DSYGSSKTAMTSRNRTGKTANNAVDSRNMGDASVGSDKNTKKHAKNSAD 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 24; DB 6; Length 215;
Pred. No. 2.03e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/238,163
FLILIG DATE: 03-MAY-1994
CLASSIFICATION: 800
                                                                                                                                                                                                            US-08-238-163-5 STANDARD; DNA; UNC; 215 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 2307E-540
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                  Sequence 5, Application US/08238163
Sequence 5, Application US/08238163
Patent No. 5569830
GENERAL INFORMATION:
                                                                                     161 AKNSADGKVGSKNNGDRNNRYGTGTK 186
                                                                                                                           488 CTAAAGCGAGCTTAGAAGCAAATGTT 513
                                                                                                                                                                                                                                                                                                                                                                      BENNEIT, Alan
LABAVITCH, JOhn M.
POWELL, Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: STOTZ, Henrik
TITLE OF INVENTION: PLANT
TITLE OF INVENTION: POLYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 15.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RY: US
94105-1493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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LOOSMORE, Sheena M
           APPLICANT:
                    APPLICANT:
APPLICANT:
                                                                                                     STREET:
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                                                                                                                                                                 TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with TITLE OF INVENTION: Reduced Protease Activity NUMBER OF SEQUENCES: 23 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2894;
  450 GCCACCTAAATATGTTGTTGCAACAATGCTACCACCTTCTGGCATTAAT 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2675 CGCTTGTTGTTGCGTCAATTCTTCTAATGATGGTTCACGCCCTT 2718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
Sequence 2894 BP; 897 A; 570 C; 515 G; 912 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 CGCTTCTGGTTGATTTAATTGTTCTAATAATTTTTCAAGCTCTT 137
                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/483,859
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 24,973
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-495 MIS:vg
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEPHONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2844 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 22; DB 7; Lt
Pred. No. 2.43e-01;
                                                                                                                                                                                                               E: Sim & McBurney
Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-472-173-1 STANDARD; DNA; UNC; 2894 BP
                                  .T 5
US-08-483-859-1 STANDARD; DNA; UNC; 2894 BP
                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
PRIOR APPLICATION NUMBER: US 08/278,091
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08472173. Sequence 1, Application US/08472173 Patent No. 566533 GENERAL INFORMATION:
                                                                       Sequence 1, Application US/08483859.
Sequence 1, Application US/08483859
Patent No. 5656436
GENERL INFORMATION:
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: XNG, Yan-Ping
                                                                                                                APPLICANT: LOOSMORE, Sheena M. APPLICANT: YANG, Yan Ping APPLICANT: YANG, Yan Ping APPLICANT: CHONG, Pele CHONG, PELCANT: KLEIN, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y Match 2.9%;
Local Similarity 75.0%;
nes 33; Conservative
                                                                                                                                                                                                             ADDRESSEE: Sim & STREET: Suite 701 CITY: Toronto STATE: Ontario COUNTRY: Canada ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1900
                                                                01-JAN-1900
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Sequence 1, Application US/08278091.

Sequence 1, Application US/08278091.

Sequence 1, Application US/08278091.

Sequence 1, Application US/08278091.

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: LOSSONER. Sheena M
APPLICANT: TOWGY. Yan-Ping
APPLICANT: OWEN, Raymond P.

APPLICANT: CHONG, Pele

APPLICANT: CHONG, Raymond P.

TILLE OF INVENTION: Analog of Haemophilus Hin47 Protein with
TILLE OF INVENTION: Reduced Protease Activity

CORRESPONDENCES 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sim & MCBUINEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                              APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with
TITLE OF INVENTION: Reduced Protease Activity
NUMBER OF SEQUENCES: 23
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2.9%; Score 22; DB 7; Length 2894;
Best Local Similarity 75.0%; Pred. No. 2.43e-01;
Matches 33; Conservative 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                   COUNTRY: Canada

ZIP: MGG 1R7

COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC Compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CLASSIFICATION NUMBER: US/08/472,173
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
PRICK APPLICATION NUMBER: US 08/278,091
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-493 MIS:VG
TELECOMMUNICATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-493 MIS:VG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2675 CGCTTGTTGTTGCGTCAATTCTTCTAATGATGGTTCACGCCCTT 2718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
Sequence 2894 BP; 897 A; 570 C; 515 G; 912 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 CGCTTCTGGTTGATTTAATTGTTCTAATAATTTTTCAAGCTCTT 137
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STREET: Suite 701, 330 University Avenue
                                                                                                                                                                                                                        E: Sim & McBurney
Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JT 7
US-08-278-091-1 STANDARD; DNA; UNC; 2894 BP.
                           CHONG, Pele
OOMEN, Raymond P.
KLEIN, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 2894 base pairs
YANG, Yan-Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                    CITY: Toronto STATE: Ontario
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SEQUENCE CHARACTERISTICS:

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88888888
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Peptide Libraries
103
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                                                                                                                                                                                                                                                                                                                                                                          Query Match

2.9%; Score 22; DB 6; Length 2894;
Best Local Similarity 75.0%; Pred. No. 2.43e-01;
Matches 33; Conservative 0; Mismatches 11; Indels
                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NORTE:
APPLICATION NUMBER: 21-JUL-1994
CLASSIFICATION: Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-371
TELEPHONE: (416) 595-1155
TELEPHONE: (416) 595-1165
TENGRATION FOR SEQ ID NO: 1: SEQUENCE CHARACTER STICS:
LENGTH: 2894 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                  2675 CGCTTGTTGCTTCGCTCAATTCTTCTAATGATGGTTCACGCCCTT 2718
                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear Sequence 2894 BP; 897 A; 570 C; 515 G; 912 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 CGCTTCTGGTTGATTTAATTGTTCTAATATTTTTCAAGCTCTT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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PCT-US95-11934-100 STANDARD; DNA; UNC; 74 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Per
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCI/US95/11934
FILING DATE: 20-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 100, Application PC/TUS9511934. Sequence 100, Application PC/TUS9511934 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIONALIA MISTOCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 100:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New York
: New York
                3: Ontario
rry: Canada
M5G 1R7
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      Toronto
                STATE: O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: N
STATE:
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4.8%; Pred. No. 8.12e-01;
ative 19; Mismatches 41; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 94, Application PC/TUS9511934.
Sequence 94, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

2.7%; Score 21; DB 13; Length 74;
Best Local Similarity 7.2%; Pred. No. 8.12e-01;
Matches 5; Conservative 19; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATUS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/VS95/11934
FILING DATE: 20-SEP-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
Sequence 74 BP; 3 A; 4 C; 3 G; 1 T; 63 other;
                                                                                                                                              MOLECULE TYPE: DNA (genomic)
Sequence 74 BP; 6 A; 6 C; 1 G; 1 T; 60 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1101-196-228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT-US95-11934-94 STANDARD; DNA; UNC; 74 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALTORATION OF THE STATE OF THE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 74 base purryPFE: nucleic acid
                                                                                                                                                                                                                                                                                                                             Similarity 4.8%;
3; Conservative
LENGIH: 74 base pairs
                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New York
: USA
                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             435 AAC 437
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                                                                                         Sequence 98, Application PC/TUS9511934.
Sequence 98, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 92, Application PC/TUS9511934.
Sequence 92, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From VMMBER OF SEQUENCES: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.7%; Score 21; DB 13; Length 81;
4.8%; Pred. No. 8.12e-01;
ative 19; Mismatches 41; Indels
                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
Sequence 81 BP; 6 A; 6 C; 4 G; 5 T; 60 other;
                                                   7I 10
PCT-US95-11934-98 STANDARD; DNA; UNC; 81 BP.
                                                                                                                                                                                                                                                                                                                                                                             1101-196-228
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PCT-US95-11934-92 STANDARD; DNA; UNC; 81 BP.
                                                                                                                                                                               ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CIIY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                        ATORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELERX: (614) PENNIE
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 81 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 4.8%;
3; Conservative
                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ry Match
Sest Local Similarity
                                                                                                                                                                                                                          USA
                    214 CITCATCGC 206
 63 BNNBNACGC 71
                                                                                                                                                                                                                                   10036
                                                                                                                                                                                                                          COUNTRY:
                                                                                    01-JAN-1900
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                                                   RESULT
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670 CITGAICAACGITACGITITAAAGGIGCACGCICITICGAITICITIAAGAAIIGIAIIGA 611
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Sequence 1, Application US/08273846.
Sequence 1, Application US/08273846.
Sequence 1, Application US/08273846.
GENERAL INFORMATION:
APPLICANT: SCHERIBER, ALAN D.
APPLICANT: PARK, JONG-GU
TITLE OF INVENTION: METHODS OF STIMULATING PHAGOCYTOSIS
NUMBER OF SEQUENCES:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINOTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                      COMPUTER READABLE FURM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSIFCATION:
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 1101-196-228
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 869-9741/8864
TELEPHONE: (212) 869-9741/8864
TELEPHONE: SEQIENCE
INFORMATION FOR SEG ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 81 base pairs
TUDE: NUMBER: NUMBER: NUMBER: NUMBER: ABTORNEE CHARACTERISTICS:
LENGTH: 81 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 21; DB 13; Length 81;
Pred. No. 8.12e-01;
18; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.

ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: FIPOPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,846
FILING DATE: 12-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
Sequence 81 BP; 3 A; 5 C; 6 G; 4 T; 63 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JT 12
US-08-273-846-1 STANDARD; RNA; UNC; 290 BP.
               ADDRESSEE: Pennie & Edmonds
STREDT: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.7%;
Best Local Similarity 11.0%;
Matches 8; Conservative
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              610 AACCACCACACC 598
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                                                                                           USA
                                                                                     COUNTRY: UZIP: 10036
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01-JAN-1900
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                                             Сp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 99, Application PC/TUS9511934.

Sequence 99, Application PC/TUS9511934.

CREERAL INFORMATION:
CAPPLICANT: Cytogen Corporation
TITLE OF INVENTION: Peptide Libraries
COUNTERP: 1155 Avenue of the Americas
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
                                                                                                                              MOLECULE TYPE: DNA (genomic)
Sequence 290 BP; 17 A; 34 C; 8 G; 11 T; 220 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.6%; Score 20; DB 13; Le 3.2%; Pred. No. 2.63e+00; ative 19; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,82
REFERENCE/DOCKET NUMBER: 1101-196-228
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
Sequence 75 BP; 1 A; 1 C; 7 G; 5 T; 61 other;
                                                                                                                                                                                       T 15
PCT-US95-11934-99 STANDARD; DNA; UNC; 75 BP
             NAME: WILSON, MARY J.

REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 555-29
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                           Insufficient Memory to reconstruct alignment
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 75 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 NNB 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                           APPLICANT: Rosenblum, Michael
APPLICANT: Rohr, William Jack
APPLICANT: Aggarwal, Bharat
TITLE OF INVENTION: Protein Structure of the Plant Toxin
TITLE OF INVENTION: Glonin
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 21; DB 9; Length 774;
Pred. No. 8.12e-01;
14; Mismatches 16; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Fulbright & Jaworski Patent Department
STREET: 1301 McKinney #5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: 1..774
Sequence 774 BP; 162 A; 64 C; 123 G; 102 T; 323 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 SOFTWARE APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05766 FILING DATE: 19910814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 19910814
CLASSIFICATION: 536
PRIOR APPLICATION: 536
PRIOR APPLICATION: 536
PRIOR APPLICATION: 536
ATTORNEY, AGENT INFORMATION:
NAME: Launer, Charlene A.
REGISTRATION NUMBER: 33,035
REFERENCE/DOCKET NUMBER: D-5195 PCT
TELECOMONICATION INFORMATION:
TELECOMONICATION INFORMATION INFORMATION:
TELECOMONICATION INFORMATION INFOR
7T 13
PCT-US91-05766-1 STANDARD; DNA; UNC; 774 BP.
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US-08-158-353-1 STANDARD; DNA; UNC; 824 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                       Sequence 1, Application PC/TUS9105766. Sequence 1, Application PC/TUS9105766 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gelonium multiforum
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.7%;
Best Local Similarity 37.5%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEVELOPMENTAL STAGE:
TISSUE TYPE: Nut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRECT: 150.
TTV: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Texas COUNTRY: USP ZIP: 77010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM:
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Gaps
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Sequence 99, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
Sequence 1, Application US/08158353.
Sequence 1, Application US/08158353
Sequence 1, Application US/08158353
Sequence 1, Application US/08158353
Sequence 1, Application US/08158353
TELE OF INVENTION: Methods for Diagnosing Early Lyme TITLE OF INVENTION: Disease
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 21; DB 7; Length 824; Pred. No. 8.12e-01; 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Indels
                                                                                                                          ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
Sequence 824 BP; 339 A; 104 C; 143 G; 238 T; 0 other;
                                                                                                                                                                                                                               COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/158,353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .T 15
PCT-US95-11934-99 STANDARD; DNA; UNC; 75 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    703 AAGAGCTTGAAAAGTTATTTGAATCAGTAAA 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  137 AAGAGCTTGAAAATTATAGAACAATTAAA 167
                                                                                                                                                                                                                                                                                                                                                                          UCT93-05
                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GARROLL, Alice O.
REGISTRATION NUMBER: 33,542
                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: UC
TELECOMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 824 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.7%;
Best Local Similarity 83.9%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                    STREET: Two Mil;
CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New York
                                                                                                                                                                                USA
                                                                                                                                                                                                                      MEDIUM TYPE:
                                                                                                                                                                                            02173
                                                                                                                                                                    MA
                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: N
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                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                Query Match

2.6%; Score 20; DB 13; Length 75;
Best Local Similarity 3.2%; Pred. No. 2.63e+00;
Matches 2; Conservative 19; Mismatches 42; Indels
                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
Sequence 75 BP; 1 A; 1 C; 7 G; 5 T; 61 other;
                                                                                     1101-196-228
APPLICATION NUMBER: PCT/US95/11934
                                   ATTORNEY/AGENT INFORMATION:
NAME: Mistock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-1
TELECOMMUNICATION INFORMATION:
TELEFAX: (512) 790-9090
TELEFXX: (512) 86-9741/8864
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 75 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: Fri Dec 5 08:14:07 1997 Job time: 55 secs.
              20-SEP-1995
                                                                                                                                                                                              nucleic acid
EDNESS: single
                                                                                                                                                                                                                               TOPOLOGY: linear
             FILING DATE: 2 CLASSIFICATION:
                                                                                                                                                                                                             STRANDEDNESS:
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

- n.a. database search, using Smith-Waterman algorithm п.а. MPsrch_nn Fri Dec 5 07:57:33 1997; MasPar time 100.32 Seconds 802.071 Million cell updates/sec lar output not generated. : uo

(1-771) from US08790043A.seq >US-08-790-043A-2 Title: Description: Perfect Score: N.A. Sequence:

1 ATGITAAAICITGAAAACAA.........GAITCCACGCAAFIAAAIAA 771 IACAAITIAGAACTITIGII........CIAAGGIGCGITAAITIAIT

TABLE default Gap 6 Scoring table:

142080 seqs, 52183452 bases x 2 Dbase 0; Query 0 STD Nmatch

Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

n-geneseq28 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 8.559; Variance 5.316; scale 1.610

istics:

SUMMARIES

Result No.	ult No.	Score	% Query Match	% Query Match Length DB	DB	Ω	Description	Pred. No
:	-	63	8.2	1047	2	010572	Human Natriuretic Pep	3.58e-23
O	~	52	6.7	1047	~	Q10572	Human Natriuretic Pep	1.56e-16
U	m	40	5.2	91	σ	051746	Oligonucleotide probe	1.42e-09
υ	4	38	4.9	204	-	N81164	Base substituted E.co	1.86e-08
	Ŋ	37	4.8	91	σ	051746	Oligonucleotide probe	6.67e-08
	ø	34	4.4	204	Н	N81164	Base substituted E.co	2.90e-06
υ	7	33	4.3	114	12	970467	Generic DNA sequence	9.99e-06
U	ω	32	4.2	114	12	070465	Generic DNA sequence	3.41e-05
υ	თ	31	4.0	114	12	070469	Generic DNA sequence	1.15e-04
U	10	30	3.9	114	12	070468	Generic DNA sequence	3.81e-04
ບ	디	30	3.9	114	12	070466	Generic DNA sequence	3.81e-04
υ	12	28	3.6	114	12	070470	Generic DNA sequence	4.05e-03
	13	25	3.2	114	12	070465	Generic DNA sequence	1.25e-01
	14	24	3.1	114	12	070470	Generic DNA sequence	3.76e-01
	15	24	3.1	114	12	070469	Generic DNA sequence	3.76e-01

10-JAN-1991

3.76e-01 1.11e+00 1.11e+00 1.11e+00	3.23e+00 3.23e+00 3.23e+00	uuu	444	144	44	juui	2244	9.13e+00 9.13e+00 9.13e+00	
Generic DNA sequence Ballast Constituent c Mixed oligonucleotide Generic DNA sequence	Mixed oligonucleotide Mixed oligonucleotide Ballast Constituent c		enc	encoding	encoding encoding	ling r ling r ling r	H. influenzae SB33 h1 HSV-1 qB and surround DC43 TSAR library gen DC43 TSAR library gen	translatede e encoding a 2591 anti	
Q70472 Q11195 Q51787 Q70468	Q46602 Q46603 O11197	Q70467 Q70466 Q70473	N50034 N50027	N50029 N50030	N50033 N50032	N50023 N50028 N50031	T10423 N71302 T13613 T13611	4921 5002 7388	712562 T109225
12 2 12 12	r r c						18 21 21 21		
114 36 39 114	330	114	501	501 501	501	501 501	2894 3871 74 81	501 534 534	2403 5746
3.00.0 0.00.0									
223 233 233	222	2222	222	700	222	555 557 557	22 22 21 21	2222	217
16 17 18 19	20	25 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	250	3 7 8 3 7 8	31	33 34 5	33.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0	4 4 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	4 4 4 2 4 5
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ALIGNMENTS

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O-APR-1991 (first entry)
Human Natriuretic Peptide Receptor B.
NPRB; ANP; BNP; CNP; kidney failure; heart failure; protein kinase; hyperaldosteronism; glaucoma; guanyl cyclase.
                                                                                                                                                    /label= extracellular domain
/note= "binds natriuretic peptides A,B and C]"
                                                                                                                                                                                                         /label = cytoplasmic domain
/label = cytoplasmic domain
/note = "GC and protien kinase activity"
/note = "GC and protien kinase activity"
/label = N-g1ycos_site
                                                                                     Location/Qualifiers
Domain 456..456
/label= transmembrane domain
Domain 479..1047
                                                                                                                                                                                                                                                                                                                                    /label= N-glycos_site
Modified -site 277..279
                                                                                                                                                                                                                                                                                                                                                          /label= N-glycos_site
Modified -site 349..351
                                                                                                                                                                                                                                                                                                                                                                                /label= N-glycos_site
Modified -site 600..602
                                                                                                /label= signal sequence
Protein 12
Protein 12
                                                                                                                                            23..455
                                                                                                                                                                                                                                                                                                                                                                                                    /label= N-glycos_site
WO9100292-A.
                                                                             Homo sapiens.
                                                                                                                                                                                                   Domain
                      010572;
                                                                                                                                            Domain
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7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   227 GITITGAGCAAATTGGTAAAGATGTTGGCAATATTGATGGTGTATATCATTCAATCGCAT 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          197 svnhnvyarnnggnnnathnnrangrnvyncgnnnmnhnnnnnanrnntngdyvnnynd 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            257 vngnsnragntratgrnwndnrtrnnananrnanntvnvntyrnnnnnynnnnrnnnr 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78 ynannsavdnknyhdndnnngngcvynaasvarnashwrnnnntagavasgnsakndhyr 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               347 TAGCTCAAGACATTAGTTCTTACTCATTAACAATTGTGGCTCATGAAGCTAAAAAATTAA 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           317 arndngvnngnsnmnnnagcnydgnnnyanvnnntnnnggtrndgnrnvnkmngrryhgv 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  407 IGCCAGAAGGIGGIAGCAIIGIIGCAACAAAAIAIIIAGGIGGCGAAIICGCAGIICAAA 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            377 tgnvvmdknndrntdnvnwamgdndsgdnnnaahysganknnwwtgrnnnwvkgannsdn 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             437 nncandnddnscdktnnstnanvangtgntnnmngvssnnnnrknmnnknnasmnwrnrw 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     525 ATTAGACTTAGGTCCTGATAATATTCGCGTTAATGCAATTTCAG-CTGGTC-CAATCCGT 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               497 nnnnngnsnryhkgagsrntnsnrgssygsnmtahg-kynnnantghnkgnvvankhvnk 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      583 ACATTAAGTGCAAAAGGTGTGGGTGGTTTCAATACAATTCTTAAAGAAATCGAAGAGGCGT 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                556 kronntrnvononkhmrdvonnhntrnngacodonnncovtnycorgsondonnndsonn 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     643 GCACCITTAAAACGTAACGTTGATCAAGTAGAAGTAGGTAAAACAGCGGCTTACTTRTTA 702
                                                                                                                    Natriuretic protein receptor B - for diagnosis and treatment of kidney failure, heart failure, hyperaldosteronism, glaucoma etc. Claim 3; Fig 1; 49pp; English.

The sequence was derived from the DNA encoding natriuretic peptide receptor B, NPRB, having quanyl cyclase (GC) activity and protein kinase activity. The DNA can be inserted into expression vectors for the proden of the protein, opt. after being mutated to produce NPRB analogues. The protein has a mol Mt. of 115 KD (calculated Mrnatriuretic peptide disorders, and also to isolate peptides using affinity chromatography. Antibodies with affinity for NPRB can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Gaps
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Human Natriuretic Peptide Receptor B.

NPRB; ANP; BNP; CNP; Kidney failure; heart failure; protein Kinase;

Hyperaldosteronism; glaucoma; guanyl cyclase.

Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  287 IIGCTAATAIGGAAGACTIACGCGGACGCITIICIGAAACIICACGIGAAGGCIICIIGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 8.2%; Score 63; DB 2; Length 1047; Local Similarity 11.4%; Pred. No. 3.58e-23; les 65; Conservative 155; Mismatches 341; Indels
                                                                                                                                                                                                                                                                                                                                                                                          51 T;
                                                                                                                                                                                                                                                                                                                                                                                       83 G;
                                                                                                                                                                                                                                                                                                                                                                                     15 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 616 dwmnrysnnndnvkgmannhnsnnsshg 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         703 AGTGACTTATCAAGTGGCGTTACAGGTG 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q10572 standard; DNA; 1047 BP.
                                                                                                                                                                                                                                                                                                                                                                                     87 A;
                                                             Goeddel D, Lowe D;
22-JUN-1990; U03586.
23-JUN-1989; US-370673.
                                           GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                 1047 BP;
                                                                                   WPI; 91-036711/05.
N-PSDB; Q10324.
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                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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55 angrannvdnrnvssnnngacsnynannsavdnknyhdndnnngngcvynaasvarnash 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 wrnnnntagavasgnsakndhyrtnvrtgnsankngnnvvtnhghnnwtaraannyndar 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             564 AATTGC-ATTAACGCGAATATTATCAGGACCTAAGTCTAATGCTAAATATTTAACATTTG 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 tddrnhyntnngvnnanngsnnsvnhnvyarnnggnnnathnnrangrnvyncgnnnmnh 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   505 CITCIAAGCICGCIT-IAGCAACACCCAICACAITAIAAIITIGAACIGCGAAIICGCCA 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235 nnnnnanrnnntngdyvnnyndvngnsnragntratgrnwndnrtrnnananrnanntvn 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   446 CCTAAATATGTTGTTGCAACAATGCTACCACCTTCTGGCATTAATTTTTAGCTTCATGA 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     295 vntyrnnnnnynnnnnrnnnrarndngvnngnsnmnnagcnydgnnnyanvnnnnn 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kidney failure, heart failure, hyperaldosteronism, glaucoma etc. Claim 3; Fig 1; 49pp; English.

The sequence was derived from the DNA encoding natriuretic peptide receptor B, NPRB, having quanyl cyclase (GC) activity and protein kinase activity. The DNA can be inserted into expression vectors for the produ. of the protein, opt. after being mutated to produce NPRB analogues. The protein has a mol Wt. of 115 kD (calculated Mr-114,952). The protein (or variants) can be used in treatment of natriuretic peptide disorders, and also to isolate peptides using affinity chromatography. Antibodies with affinity for NPRB can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Natriuretic protein receptor B - for diagnosis and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 6.7%; Score 52; DB 2; Length 1047; Best Local Similarity 9.5%; Pred. No. 1.56e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 382; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 T;
                                                                                                                  'note= "binds natriuretic peptides A,B and C]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83 G;
                                                                                                                                                                                       /label= cytoplasmic domain
/note= "GC and protien kinase activity"
Modified -site 24..26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 C;
   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative 166;
                                                                                                                                   Jonain 456..456
Jabel transmembrane domain
Jonain 479..1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87 A;
                                                                                                  'label= extracellular domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GETH ) GENENTECH INC.
Chang M, Goeddel D, Lowe D;
WPI; 91-036711/05.
                                                                                                                                                                                                                                     /label= N-glycos_site
Modified -site 35.37
/label= N-glycos_site
Modified -site 161.163
                                                                                                                                                                                                                                                                                                                                                                                                         /label N-glycos_site
Modified -site 349.351
/label N-glycos_site
Modified -site 600.602
                                                                                                                                                                                                                                                                                                                               .197
                                                                                                                                                                                                                                                                                                                                             /label= N-glycos_site
Modified -site 244..246
                                                                                                                                                                                                                                                                                                                                                                            /label= N-glycos_site
Modified -site 277..279
                                'label= signal sequence
                                                                                       23..455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-JUN-1990; U03586.
23-JUN-1989; US-370673.
                                                                                                                                                                                                                                                                                                         'label = N-glycos_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= N-glycos_site
                                                                    /label= mature NPBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1047 BP;
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                                                                                                                                                                                                                                                                                                                                                             Modified -site
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                                               415 nknnwwtgrnnnwvkgannsdnnncan-dnddnscdktnnstnanvangtgntnnmngvs 473
                                                                                             268 CACCATCAATATTGCCAACATCTTTACCAATTTGCTCAAAACCATTAATAACCTCTTCAT 209
                                                                                                                                                                                    534 ynnnantghnkgnvvankhvnkkrnnntrnvnnnnkhmrdvnnnhntrnngacndnnnnc 593
                                                                                                                                                                                                                                         594 nvtnycnrgsnndnnnndsnnndvmnrysnnndnvkgmannhnsnnsshgsnkssncvvd 653
                                                                                                                                  474 snnnnrknmnnknnasmnwrnrwnnnngnsnryhkgagsrntnsnrgssygsnmtahgk 533
                                                                                                                                                            208 CGCTTTGAACATCAATTTGATATAAGTGCGCTTCTGGTTGATTTAATTGTTCTAATAATT 149
                            355 ggtrndgnrnvnkmngrryhgvtgnvvmdknndrntdnvnwamgdndsgdnnnaahysga 414
 386 GCCACAAITGITAATGAGTAAGAACTAATGTCTTGAGCTAACAAGAAGCCTTCACGTGAA 327
                                                                                                                                                                                                             148 TTTCAAGCICITTACGGCTACGTICITIACGGTAAGTAAATACTAATITAGCACCTAATT 89
                                                                                                                                                                                                                                                                 88 GATCTAAAACTTTAGCGACACCAAAAGCAATACTACGCTTATTAGCGATTCCCATGATGA 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-NOV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment, base substitutions; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         claim 3; Page 14; 23pp; English.

claim 3; Page 14; 23pp; English.

difforncleotide probe MK14A consists of nucleotides 5-95 of MK14
(Q51735). It hybridized to all spp. of mycobacteria tested, but
cross reacted to a few non-mycobacterial spp. The probe may
be useful as an initial screen for mycobacterial infection.
See also Q51735-45 and Q51747-59.
Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        458 GCGAATTCGCCACCTAAATATGTTGTTGCAACAATGCTACCACCTTCTGGCATTAA 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 gssvhsyyvvhvvshhhsvhhvvhhvhvsvvvvhhvvhvvhhvhyhvyvsvctcaa 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New olign:nucleotide probes specific for Mycobacteria - used for detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                                                                                                                                               Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.2%; Score 40; DB 9; Length 91; 7.1%; Pred. No. 1.42e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
19..69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function-multiple cloning site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N81164 standard; DNA; 204 BP
                                                                                                                                                                                                                                                                                                                                                                                                      31-MAY-1994 (first entry)
Oligonucleotide probe MK14-A
                                                                                                                                                                                                                                                                                                                                                                              Q51746 standard; cDNA; 91 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BECT ) BECTON DICKINSON CO. Shank DD, Spears PA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAY-1992; US-889651.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                654 srnvnkntdyg 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-1993.
24-MAY-1993; 108325
                                                                                                                                                                                                                                                                                                                           28 CATATGTTTG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 93-378844/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N81164;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                samples
                                                                                                                                                                                                                                                                                                                                                                                            051746;
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                                                                                                                                          Introducing random point mutations into nucleic acods -
by prepn of single stranded template, annealing a primer, elongation,
misincorporation, completion of molecules and screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                  Random point mutations were introduced into the alpha fragment of E.coli beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligonuclectide was hybridised to it to generate a popp of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and them objects are a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14 (Q51735). It hybridized to all spp. of mycobacteria tested, but cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also 051735-45 and 051747-59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New oligo:nucleotide probes specific for Mycobacteria - used for detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 T; 108 Others;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
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                                                                            (SUSO) SUOMEN SOKERI OY.
Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.9%; Score 38; DB 1; Length 204; 13.5%; Pred. No. 1.86e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.8%; Score 37; DB 9; Length 91; 2.0%; Pred. No. 6.67e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 dhyvybbbvynvhnhnncncccbnnhvchnvhbnnh 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               358 IGICITGAGCIAACAAGAAGCCITCACGIGAAGIII 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47 C; 17 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    occurred singularly in any given mutant. See also P80575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Page 14; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAY-1994 (first entry)
Oligonucleotide probe MK14-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T 5
Q51746 standard; cDNA; 91 BP.
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01-DEC-1993.
24-MAY-1993; 108325.
25-MAY-1992; US-889651.
(BECT ) BECTON DICKINSON CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 13.5%;
Matches 13; Conservative
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                                                                                                                                                                                                                                          Disclosure; p; English.
                                                     US-034819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shank DD, Spears PA;
WPI; 93-378844/48.
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Best Local Similarity
05-MAY-1988.
30-MAR-1988; 105163.
                                                                                                                                 WPI; 88-279927/40.
                                                     03-APR-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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31-JAN-1994; US-189331

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Introducing random point mutations into nucleic acods -

by prepn of single stranded template, annealing a primer, elongation,

misincorporation, completion of molecules and screening.

Disclosure; p; English.

Random point mutations were introduced into the alpha fragment of

E.coli beta-galactosidase. The wild type sequence was obtained as a

coli beta-galactosidase. The wild type sequence was obtained as a

it to generate a popn of DNA molecules which terminate at all

possible nucleotide positions within a specified region. The

variable 3' ends generated in this way are used as primers for

reverse transcriptase. Nucleotides are misincorporated by the

camplified and then molecules are completed to forms that can be

many and the molecules are completed to forms that can be

The sequence covers all 176 difft base substitutions, most of which

securred singularly in any given mutant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 cgymrttthhyrrmrbnvyrdynrsdaaawyccyrrsvkydccynachhddhyvybbbvy 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 CGCTAATAAGCGTAGTATTGCTTTTGGTGTCGCTAAAGTTTTAGATCAATTAGGTGCTAA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G5-APR'1995 (first entry)
Generic DNA sequence to generate a random TSAR petide library.
TSAR: totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                           08-NOV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 T; 108 Others;
                                                                                                                                                                                                                                                            03-APR-1987; US-034819.
(SUSO) SUOMEN SOKERI OY.
Lehtovaara P. Knowles J. Koivula A. Bamford J. Reinikainen T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 34; DB 1; Length 204;
Pred. No. 2.90e-06;
54; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144 nvhnhnncncccbnnhvchnvhbnnhrnwayvrhdarrddvh 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence represents 'Z'; Z can be a ', 9 or 12 nucleotides (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204 BP; 21 A; 47 C; 17 G;
                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers 55..60
                                                                                                                                                            function-multiple cloning site
             N81164 standard; DNA; 204 BP. N81164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q70467 standard; DNA; 114 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Conservative
                                                                                                                                                                                   187..204
                                                                                                                                  19..69
                                                                                                                                                                                                                                                30-MAR-1988; 105163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                               Lehtovaara P, Know]
WPI, 88-279927/40.
                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence of 6,
                                                                                                                                                                                                               EP-285123-A.
                                                                                                                                                                                 primer_bind
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/note= "this
                                                                                                                                                                                                                                 05-MAY-1988
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                                                                                                                                                /*tag=
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RESULT
                 444855555555555555
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US-013416

30-DEC-1993;

01-FEB-1994; U00977. 01-FEB-1993; US-0134

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Discussure; regges 33, 232pp; English.

CO 70467 is a generic DNA sequence used to generate random TSAR (Totally CO 70467 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in 070466-68.

CO ther specific peptides generated by these generic sequences are shown in comprising at least two functional regions - a binding domain with comprising at least two functional regions - a binding domain with a finitity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker comprise between the 2 domains. The oligonuclectides are also designed in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs or compers on confers on biologically active moiety, eg. metal ion, can companie a chemically or biologically active moiety, eg. metal ion, calling a TSAR binding domain can be used in vivo can also replace the function of macromolecules, eg. complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing sequence 114 BP; 0 A; 2 C; 2 G; 2 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Generic DNA sequence to generate a random TSAR petide library. TSAR: totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker;
                                                                                          Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain proteins page 35; 255pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        direct; rapid; detection; screening; treatment; generic; ss. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 33; DB 12; Length 114
Pred. No. 9.99e-06;
31; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              580 GGATTGGACCAGCTGAAATTGCATTAACGCGAATATTATCAGGACCT 534
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sequence of 6, 9 or 12 nucleotides (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JT 8
Q70465 standard; DNA; 114 BP.
                    (UYNC-) UNIV NORTH CAROLINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 4.3%;
Local Similarity 3.7%;
les 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-DEC-1993; US-176500
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-APR-1995 (first entry)
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P-PSDB; R65150 and R65151.
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                                    Fowlkes DM, Kay BK;
WPI; 94-279739/34.
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/note= "this sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kay BK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        776000
                                                                          P-PSDB; R65153.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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promprising a binding domain and an effector domain

Disclosure, Page 35, 255pp; English.

Cy 70465 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be constructed as follows: X(NNB)6(TGC)(NNB)112(NNB)14(TGC)(NNB)3Y. X and Y are flanking restriction sites (X is not the same as Y) that are constructed to the specified further. Other generic sequences are shown in 070466-68.

CC and Y are flanking restriction sites (X is not the same as Y) that a recomprising at least two functional regions. - a binding domain with comprising at least two functional regions. - a binding domain with affailty for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker of peptide between the 2 domains. The oligonuclectides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs or comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion, cadiover a chemically or biologically active moiety, eg. metal ion, confer suchods to peptide, toxin or enzyme, to the specific target or on the monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process.

Sequence 114 BP: 0 A: 2 C; 2 G; 2 T;
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identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain proteins comprising a binding domain and an effector domain proteins of pisclosure; Page 35, 255pp; English.

70469 is a generic formula can be represented as follows: X[TGC) (NNB) LOTTH (TGC) (NNB) (T
                                                                                                  070469;
07-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR peptide library
Generic DNA sequence to filmity reagent; synthetic; binding domain;
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
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/note= "this sequence represents 'Z'; Z can be a
sequence of 6,9 or 12 nucleotides (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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070469 standard; DNA; 114 BP.
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US-189331.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1994; U00977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fowlkes DM, Kay E
WPI; 94-279739/34.
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30-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
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RESULT
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generated by these generic sequences are shown in R65150-54. TSARS are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 dysteine residues positioned in, or flanking, the upredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARS or compens. comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active modety, eg. metal ion, radioisotope, peptide, toxin conformation of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma conformation or in vivo antibody production. The TSARS are easily
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               676 CITCIACITGAICAACGITACGITITAAAGGIGCACGCICITCGAITICITIAAGAAITG 617
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                                                                                                                                                                                                                                                                                                                                                                                                                            4 G;
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Best Local Similarity 5.4%;
Matches 6; Conservative
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DECOURGE Standard; DNA: 114 BP.

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onfer some degree of conformational rigidity to the peptides. These residues confer some degree of conformational rigidity to the peptides. The TSARS decliver a chemically or biologically active molety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the monclonal or polyclonal antibodies and therefore circumvent the need production. The TSARS are easily characterised and have designed activity allowing direct and rapid detection in a screening process.
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667 GATCAACGTTACGTTTTAAAGGTGCACGCTCTTCGATTTCTTTAAGAATTGTATTGAAAC 608 3 ԽոսԽողծողծողծողծողծողծողծողծողծութեց հայաստողութութութութութութութութութ 62 0; Gaps Length 114; 32; Mismatches 77; Indels Pred. No. 3.81e-04; Score 30; DB 12; 3.9%; 2.7%; Conservative Local Similarity Query Match Matches g

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63 baabaabaabaabaabaabtgcaabaabaabaabaabaabaabaabaab 114 607 CACCCACACCTITIGCACTIAATGTACGGATIGGACCAGGTGAAATIGCAIT 556 ģ

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Tidentifying proteins or peptide(s) which bind a ligand - by recening a recombinant vector library expressing fusion proteins or comprising a binding domain and an effector domain by screening a recombinant vector library expressing fusion proteins or comprising a binding domain and an effector domain bisclosure; Page 35; 255pp; English.

CO 70466 is a generic DNA Sequence used to generate random TSAR (Totally represented as follows:X(NNB)10TGC(32(NNB)4Z(NNB)8(TGC)(NNB) (TCC)2(NNB)10TGC(32(NNB)4Z(NNB)8(TGC)(NNB) (TCC)2(NNB)10TGC(32(NNB)4Z(NNB)8(TGC)(NNB) (TCC)2(NNB)10TGC(32(NNB)4Z(NNB)8(TGC)(NNB) (TCC)2(NNB)10TGC(32(NNB)4Z(NNB)8(TGC)(NNB) (TCC)2(NNB)10TGC(32(NNB)4Z(NNB)8(TGC)(NNB) (TCC)2(NNB)10TGC(32(NNB)4Z(NNB)8(TGC)(NNB) (TCC)2(NNB)10TGC(32(NNB)4Z(NNB)4Z(NNB)4Z(NNB) (TCC)2(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(NNB)4Z(
                                                                                 Generic DNA sequence to generate a random TSAR-9 petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
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/note= "this sequence represents 'Z'; Z can be a
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070466 standard; DNA; 114 BP.
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30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UVNC-) UNIV NORTH CAROLINA.
                                                      05-APR-1995 (first entry)
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WPI; 94-279739/34.
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01-FEB-1994; U00977.
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Gaps

688 CIGITITACCIACIICIACIIGAICAACGIIACGIIIIAAAGGIGCACGCICIICGAIII 629

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28; Mismatches 67; Indels

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Tidentifying proteins or peptide(s) which bind a ligand - by recenting a recombinant vector library expressing fusion proteins or comprising a bluding domain and an effector domain proteins or screening a recombinant vector library expressing fusion proteins or screening a recombinant vector library expressing fusion proteins of scales of 255pp; English.

CC 970470 is a generic DNA Sequence used to generate random TSAR (Totally CS Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB)4(CAC)(NNB)8(NNB)6(CAC)(NNB)8 (CC CAC)2(NNB)Y. X and Y are flanking restriction sites (X is not the same of sequences (970471-73) have invariant histidine residues incorporated into variant sequences. TSARs are concatenated control or sequences. TSARs are concatenated into variant sequences. TSARs are concatenated control or peptides, comprising at least two functional creditor peptide portion that is chemically for a ligand and a second effector peptide portion that is chemically or biologically active. They comprise a linker peptide between the 2 domains. The TSARs of linker peptide between the 2 domains. The TSARs of linker peptide toxin or engage or on the concolouse or polyclonal antibodies and therefore circumvent the need for complex mathods of purity of which the mental for the complex mathods of purity of complex mathods of purity of complex mathods.
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complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process. Sequence 114 BP; 0 A; 4 C; 4 G; 4 T;
                                                                                                                                                                                                                                494 GCTTTAGCAACACCCATCACATTATAATTTTGAACTGCGAATTCGCCACCTAAATATGTT 435
                                                                                                                                                                                           5 gcnnbnnbnnbnnbnnbnnbnnbnnbnnbtgctgcnnbnnbnnbnnbnnnnnnbn 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Generic DNA sequence to generate a random TSAR peptide library.

TSAR: totally synthetic affinity reagent; synthetic; binding domain; effector domain; concatenated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                              0; Gaps
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                                                                                                                                                                                                                                                                                                                     434 GITGCAACAAIGCIACCACCTICIGGCAITAAITITITAGCITCAIGAGC 385
                                                                                                                      Length 114;
                                                                                                                                                         28; Mismatches 74; Indels
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/note= "encoded by Z (see comments)"
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Q70470 standard; DNA; 114 BP.
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larity 7.3%;
Conservative
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31-JAN-1994; US-189331
                                                                                                                                 Local Similarity
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Q70470 standard; DNA; 114 BP.
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Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins screening a recombinant vector library expressing fusion proteins. Disclosure; Page 35: 255pp; English.

070465 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB)6(TGC)(NNB)11Z(NNB)14(TGC)(NNB)3Y. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in Q70466-68. Other specific peptides generated by these generic sequences are shown in R6515-54. TSARs are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with a second effector peptide portion that is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cystains residues positioned in, or flanking, the unpredicted variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs or companising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active molety, eq. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the coll. They can also replace the function of macromolecules, eq. on the monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                             Generic DNA sequence to generate a random TSAR petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
Synthetic.
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Pred. No. 1.25e-01;
25; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 banbanbanbanbanbanbanbanbanbanbanbtgcanbanb 111
                    63 banbanbanbanbanbcacanbanbanbanbanbanb 102
                                                              628 CITTAAGAATIGIATIGAAACCACCCACACCTITIGCACI 589
                                                                                                                                                                                                                                                                                                                                                                           /*tag= a /note= "this sequence represents ^{2}; ^{2} can be sequence of ^{6}, ^{9} or ^{12} nucleotides (see
                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
55..60
                                                                                                                                                    Q70465 standard; DNA; 114 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UNNC-) UNIV NORTH CAROLINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 3.2%;
Best Local Similarity 5.8%;
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P-PSDB; R65150 and R65151.
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01-FEB-1994;
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Tentifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins or comprising a binding domain and an effector domain bisclosure; Page 36: 255pp; English, and the screening a generic DNA sequence used to generate random TSAR (Totally Disclosure, Page 36: 255pp; English, proteins generic formula can also be cropresented as follows: X(NNB)4(CAC)(NNB)4(CAC)(NNB)8Z(NNB)6(CAC)(NNB)8Z(NNB)6(CAC)(NNB)8Z(NNB)7. X and Y are flanking restriction sites (X is not the same other generic sequences (Q70471-73) have invariant histidine residues other generic sequences (Q70471-73) have invariant histidine residues incorporated into variant sequences. TSARs are concatenated by this and other generic sequences. TSARs are concatenated by the crospinal proteins or peptides, comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The TSARs or comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active modety, eg. metal too.

C call. They can also replace the function of macromolecules, eg. call. They can also replace the function of macromolecules, eg. metal too.

C coll. They can also replace the function of macromolecules, eg. contained the too of the production in vivo antibody of production. The TSARs are easily characterised and have designed and account of the production of the production in vivo antibody of this production in vivo antibody and account of the production in vivo anti
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TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concatenated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
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Pred. No. 3.76e-01;
23; Mismatches 60; Indels
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/note= "this sequence represents '2'; 2 can be
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/note= "encoded by Z (see comments)"
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(UYNC-) UNIV NORTH CAROLINA.
Fowlkes DM, Kay BK;
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Local Similarity 5.7%;
Nes 5; Conservative
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10-APR-1995 (first entry)
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01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
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GITICAAIACAAIICITAAAGAAAICGAAGAGCGIGCACCIII 650

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Matches

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PR 30-DEC-1993; US-013416.

PR 30-DEC-1993; US-013416.

PR 31-DR-1993; US-105606.

PR 51-DR-1994; US-189331.

PR 51-DR-1994; US-189331.

PR 51-DR-1994; US-189331.

PR 61-DR-1994; US-189331.

PR 61-DR-1994; US-189331.

PR 61-DR-1994; US-189331.

PR 61-DR-1994; US-189331.

PR 7 Comprising binding domain and an effector domain proteins of proteins a pencic DNA sequence used to generate random TSAR peptide C 7050 (NNB) 52 (NNB) 12 (TGC); UNB) 14 (TGC); Y. X and Y are flanking restriction This generate pertains perfected to the same as Y) that are not specified further. This sequences are shown in 707465-68. Other specific peptides concatenated by these generic sequences are shown in R65150-54. TSARs are concatenated by these generic sequences are shown in R65150-54. TSARs are generated by these generic sequences are shown in R65150-54. TSARs are concatenated by these generic sequences are shown in R65150-54. TSARs are offector peptide portion that is chemically or biologically active residues positioned in, or flanking, the contains 2 or 4 cysteine residues positioned in, or flanking, the conformational rigidity to the peptides. These residues confer some degree of conformational rigidity to the specific target or on the cell. They can also replace to the functional active moiety, eg. metal ion, radiolsotope, peptide, toxin conformation of macromolectules, eg. monoclonal or polyclonal antibodies conferences are said activity allowing direct and rapid detection in a screening process.
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sequence of 6,9 or 12 nucleotides (see
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                                                                 18-AUG-1994.
01-FEB-1994; U00977.
8888888888888888888888
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1; Gaps 1; Query Match 3.1%; Score 24; DB 12; Length 114; Best Local Similarity 6.3%; Pred. No. 3.76e-01; Matches 7; Conservative 28; Mismatches 75; Indels

1 tgcnnbnnbnnbnnbnnbnnbnnbnnbnnbtgcnnbnnbnnbnnbnnbnnbnnbn

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Search completed: Fri Dec 5 07:59:19 1997 Job time: 106 secs.

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Release 2 Copyright Di	. 2.1D John F. Collins, Biocomputing Research Unit. ht (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.
MPsrch_nn n.a.	- n.a. database search, using Smith-Waterman algorithm
on:	Fri Dec 5 07:44:28 1997; MasPar time 750.09 Seconds 1128.898 Million cell updates/sec
lar output no	
Title: Description: Perfect Score: N.A. Sequence: Comp:	>US-08-790-043A-2 (1-71) from US08790043A.seq 771 1 AIGHTAAATCHGAAAACAAGATHCCACGCAATHAAAHAA 771 TACAAITHAGAACTTTGITCTAAGGIGCGITAATIATT
Scoring table:	TABLE default Gap 6
Nmatch STD:	Dbase 0; Query 0
Searched:	362067 seqs, 549138275 bases x 2
Post-processing:	Minimum Match 0% Listing first 45 summaries
Database:	embl-new3 1:BCT 2:FUN 3:GEN1 4:GEN2 5:HTG1 6:HTG2 7:HUM 8:INV 9:ORG 10:MAM 11:VRT 12:PLN 13:PRO 14:ROD 15:SYN 16:UNC
Database:	9erbands) 9erbands) 18:BCT1 19:BCT2 20:BCT3 21:BCT4 22:BCT5 23:BCT6 24:BCT7 25:BCT8 26:BCT9 27:BCT10 28:BCT11 29:GEN1 30:GEN2 31:GEN2 32:BCT9 27:BCT10 28:BCT11 29:GEN1 30:GEN2 31:GEN2 33:BCT8 26:BCT9 27:BCT10 28:BCT11 29:GEN1 30:GEN2 37:INV3 38:INV4 39:INV5 40:INV6 41:INV7 42:INV8 43:INV9 44:INV10 45:INV11 46:MAM1 47:MAM2 48:MAM3 49:VRT1 50:VRT2 51:VRT3 52:VRT4 53:PR15 47:MAM3 49:VRT1 50:VRT2 51:VRT3 52:VRT4 53:PRN2 65:PRN3 65:PRN5 65:PRN6 65:PLN7 66:PLN8 67:PLN9 68:PLN1 60:PRN2 61:PRN3 62:PRN1 77:PRN5 75:PRN5
טמרמטמפי.	JUDGAR NEWS 106:BL 107:GEN1 108:GEN2 109:HTG1 110:HTG2 111:INV 112:MAM 113:YRT 114:PHG 115:PLN 116:PRI1 117:PRI2 118:ROD 119:SYN 120:UNA 121:VRL
Database:	99 t1
Statistics:	Mean 10.783; Variance 5.167; scale 2.087

Result No.	Score	Query	Length	DB	ID	Description	Pred. No.
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			190	7	ECENVMACE	gen	146-1
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12		'n.	165	~	STYENVM	rium env	4.69e-1
13		m.	35		OFU89259	allax 57k	1.26e-03
14		ω.	35	Н	OFU89259	Oxytricha fallax 57kD	1.26e-
15		ω.	140	C	MYCSEQB	bovine gr	1.26e-0
16		٣,	145	N	MYCSEQE	Mycoplasma mycoides g	1.92e-0
17		w.	146	a	MYCSEQF	Mycoplasma mycoides g	
18		Э.	152	CA	MYCSEQA	Ĕ	
19		ω.	5	ហ	128278	Sequence 5 from paten	
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23		m,	25	(*)	DDAHCH	D. discoideum mRNA fr	٠.
24		ω,	119	w	S74167	Whll=switch-regulated	•
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26		m.	134	Ψ	SCYNL203C	S.cerevisiae chromoso	•
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29		m.	43.	-	HSLAZ3	.sapiens LAZ3/BCL6	9.38e-01
30		ω.	351	w	SCXIVL	S.cerevisiae DNA of c	-
c 31		w.	2	.,	I28278	Sequence 5 from paten	
32		'n.	118		HUM33DPTP	Human 33-kDa phototra	
33		'n	14(MYCSEQC	Mycoplasma capricolum	
34		'n	269		CET07F10	Caenorhabditis elegan	•
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36		m	36	٠,	SDFNBBA	e fnbB	
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LIOCUS
ANABEFA 4142 bp DNA BCT 18-AUG-1993
DEFINITION Anabaena sp. sequence-specific DNA binding protein (bifA) gene,
COMPLETE CGS.
ACCESSION 110036
NULD 514008
NETWOORD DNA binding protein; bifA gene.
NORGANISM Anabaena sp. (library: PCC 7120) DNA.
ONGANISM Anabaena sp. (library: PCC 7120) DNA.
AUTHORS Mai, T.-F., Ramasubramanian, T.S., Pu,F. and Golden, J.W.
AUTHORS Wei, T.-F., Ramasubramanian, T.S., Pu,F. and Golden, J.W.
AUTHORS Wei, T.-F., Ramasubramanian, T.S., Pu,F. and Golden, J.W.
AUTHORS Wei, T.-F., Ramasubramanian, T.S., Pu,F. and Golden, J.W.
ANABAENCE I (bases 1 to 4142)
AUTHORS Mai, T.-F., Ramasubramanian, T.S., Pu,F. and Golden, J.W.
Anabaena sp. strain PCC 7120 bifA gene encoding a sequence-specific DNA-binding protein cloned by in vivo transcriptional interference selection
JOURNAL J. Bacteriol. 175, 4025-4035 (1993)
MEDLINE J3308081 Location/Qualifiers
SOURCE //Organism="Anabaena sp."
//tissue_lib="PCC 7120"
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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FEATURES
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APIEQVEQALKENPELSMLMLRGLSSRILQTEMMIETLAHRDMGSRLVSFLJILCRDF
GVPCADGITTDLKLSHQAIAEAIGSTRVTVTRLLGDLREKKMISIHKKKITVHKPVTL
                                                                                                                                                                                          AVLVTILTGGLVSATTLAILFIADEGLRKGVFELEDIOKDLRQKREQLKVAEEQKTOV
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                                                                                                                                                               /translation="MTTGYILIAAILILGGVIATVGDRIGTRVGKARLSLFNLRPKNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MIVTQDKALANVFRQMATGAFPPVVETFERNKTIFFPGDPAERV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MOISDYPQLNLSSVPRIASVHRITGETNVQVTVNLDGTGICKAA
TGIPFLDHMLHQISSHGLIDLDVQAKGDWEIDDHHTVBDVGTTLGQALAKALGDRKGI
VRFGNFLAPLDEALVQVALDFSGRPHLSYGLQIPTERVGTYDTQLVREFFVALVNHSQ
MTLHIRQLDGINSHHIIEATFKAFARAARMALEVDPRRAGTIPSSKGVL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YLPDERGKFEKKVSELVEPLARSLFLECNVQNDEQIOSTFDTIRDKWGRLDILIHCLA
FANRDDLTGDFSQTSRAGFATALDISTFSLVQLSGAARCLMTEGSITTLSYLGGVRA
VPNYNVMGVAKAGLEASVRXLASELGSQNIRVNAISAGPIRTLASSAVGGILDMIHHV
EQVAPLRRTYTQLEVGNTAAFLASDLASGITGQVLYVDAGYEIMGM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MOSFIDIPDFQLTTKNTPSVVMTSDLRKVYRIGFWMNQKVVSLK
GCSLTVYQGETFGLLGPNGAGKTTLLKLLGIIRPSGGKGLLLGQPLGDX"
1 909 c 858 g 1242 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation="MTTKISMLNLTGKNALVTGIANNRSIAWGIAQQLHAAGANLGIT/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Shows 70.2% similarity and 48.6% identity to the EnvM protein of Salmonella typhimurium"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="shows 67.3% similarity and 50.5% identity to the HisB protein of Azospirillum brasilense"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2327 atgttcaaaatgatgaacaaattcagtctacttttgataccatccgcgataaatggggca 2386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2447 ttagccaaacatctcgtgctggttttgccacggctttagatatcagcactttttcactgg 2506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     197 AIGTICAAAGCGAIGAAGAGGITATIAAIGGITITICAGCAAATIGGIAAAGAIGITGGCA 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           377 CAATTGTGGCTCATGAAGCTAAAAATTAATGCCAGAAGGTGGTAGCATTGTTGCAACAA 436
complement(<1.498)
/note="No homologous sequence was found in GenBank"</pre>
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                                                                                                                                                                                                                                                                                                                                                               /product="DNA-binding protein"
/db_xref="PID:g142009"
/transl_table=11
                                                                                                             _xref="PID:9289134"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="PID:g142010"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="PID:g142011"
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                                                     /codon_start=1
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/label=ORF2
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les 333; Conservative
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Substitution of the protein 132; ABC transporter; Mg-chelatase subunit; Na/H antiporter; Path protein; Pleb; UDP-3-0-acyl
Na/H antiporter; Path protein; Pleb; UDP-3-0-acyl
Na/H antiporter; Path protein; Pleb; UDP-3-0-acyl
Na/H substitution of the protein protein; Protein; Protein; C-type cytochrome synthesis protein; cell division protein; FrsH; cobyrinic acid a,c-diamide synthase; protein; cell division enoyl-leayl-carrier-protein] reductase; esterase; extracellular nuclease; fmu and fmw protein; glucose dehydrogenase-B; glutamate protein; lipoic acid synthease; lipophilic protein; protein; long-chain-fatty-acid CoA synthease; methyl-accepting chemotaxis protein; photosystem I PsaM subunit; requiatory components of sensory transduction system; regulatory protein for beta-lactamase; sensory transduction histidine kinase; spore protein sp21; sulfur deprivation response regulator; tRNA-Arg; thiamin biosynthetic virulence associated protein B; virulence associated protein C; Synechocystis sp. (strain:pCC6803) DNA.

Synechocystis sp. (strain:pCC6803) DNA.
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Submitted (28-JUN-1996) to the DDBJ/EMBL/GenBank databases. Satoshi
Tabata, Razusa DNA Research Institite, Laboratory of Gene Structure
2; 1523-3, Yanauchino, Kisarazu, Chiba 292, Japan
(E-mail:tabata@kazusa.or.jp, Tel:+81-438-52-3933,
Fax:+81-438-52-3934)
2567 catatttgggtgtgttagagctgttcctaactacaacgttatgggagtagccaaagccg 2626
                                                                                                                                                                                                                                                                 2687 acgccatctctgctggccccatccgcaccttggcttctagtgccgttggtggcattttag 2746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gattagaagctagtgtacgttatctagcatctgaactcggctctcaaaatattcgcgtta 2686
                                                                                                                                                                                                                                                                                                                                                                                                  2747 atatgattcatcatgtggagcaagtagcccccttacgtcggactgtgactcagctagaag 2806
                                                                                                                                                                                                   497 GCTTAGAAGCAAATGTTAAAATATTTAGCATTAGACTTAGGTCCTGATAATATTCGCGTTA 556
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Synechocystis sp. PCC6803 complete genome, 4/27, 402290-524345.
D90902
                                                                  437 CATATITAGGIGGCGAATITCGCAGTICAAAATIATAATGTGATGGGTGTTGCTAAAGCGA 496
                                                                                                                                                                                                                                                                                                                                    557 AIGCAAITICAGCIGGICCAAICCGIACAITAAGIGCAAAAGGIGIGGIGGITICAAIA 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 677 TAGGTAAAACAGCGGCTTACTTRITAAGTGACTTATCAAGTGGCGTTACAGGTGAAATA 736
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1 (bases 1 to 122056)
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GILGNYYVQSGDDLTTPIKYLGEAFDNNLGNWQALAAETVQGVNQVLWQNLNTNQIGV
WNSSADWNWISSSVFEAGSPQAIAQAGIFGVDLNAVI"
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GSSFSTASDIRMGDTINNLTGVLSYQWAGNASSGATWRVRSAVDGTNOFTKVNDRPVT
PENVGGSLKVTGFNVLNYFKTIDLSGVSTAIGQDPRGADTTAEFDRQTDKLVTALLAI
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EWGINADEADALDYNLDFGRDVNIFDGTVPYRSSDHDPIIVGLNLASPVEPIANEIGV
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EHIADVDESKLKEAKTYLESLVGOVPPGIEWKVEVSSVRYVDLVNOLVBOBRIDLIIN
BWPRSRLESSKLFGSHTLSLAKSTKVPVMILRPQLVSTTYTVEEMALRCQHLWRNLLVP
YDASSAGNYLIERLKSALEKAPPGKVESCYFLSILEDGMRRPELLETRRQBABAKLAE
IKQQFSPLVPNIITEVRHGSPVQEILDTAFVNDITAIAVASRRATLLDWTVPSLTDSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIVDYFGEIGIDGTGRPWEHLDGWAYRNNGALPSSTFNASEWTFSGVDALDDDAANVN
ATATPSWPIASFSAGGTNGLDLSTYVRIGRYDLPVPTRTVAPPAGSELALEVSAITYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDTNTLEVLGDEGTAIVEIDKRGQLISSMTLTAGDFADPEGLTYVGNGQFVLVEERLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TEGEDLILLDYMMPGISGYEYCRMIRASARWHALPIIMYTALDSKLSLANCLAAGADD
FISRPINGLELQARIQAMLRLKHQYDALGNLLQQRESMYHMIVHDLRNPLTNLILGIQ
VLQRSHSDAPLPPERLDRLLQAGQQIQHLVDDMLVVSKQEHGKIRLDYQEVDLLALMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TVLDDYEAIASQKOLTLVRTWENKPLVAKIDPPIFQRIÏSNLLSNAIKESPTGAKVEV
AIITEDKDKVTICFIDQGPGIKDELKIKIFEPYEVGTIMPNIAQIGLGLAFCKNMSEA
HGGAITVQDNQPRGAMFSLTLPQHPPVPFGWMPHDQWRGAAVDIGK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MSNLIITGIIDGPLPGGLPKAIELYVLADIADLSMYGIEAATNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NASTGPEFTLSGSATAGDYIYVASETSGFNSFFGFNPNFTDGVANINGDDTILLFENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_table=11
/translation="MGTASILVADDDFDNFDVIDALLADQGYELNYADSGQRAIDNLD
                                                                                                                                                                                                                                                                    sensory transduction
                                                                                                                                                                                                                                                                    'product="regulatory components of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="extracellular nuclease"
/db_xref="PID:91652030"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="hypothetical protein"
/db_xref="PID:g1652029"
/organism="Synechocystis sp."
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/note="ORF_ID:s110654"
                                                                                                                                                                                                                                                                                                                                                                                  /db_xref-"PID:g1652028"
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/gene="nucH"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="ORF_ID:s1r0670"
                                                                                                                                                                 /note="ORF_ID:slr1400"
                                              /strain="PCC6803"
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Elvygvvrrqrtldclieqigdrpptgrqppdlrtyqlgtyqlrydgypasaavnyg
VDARARQFKGLSKVVRQMLERRQAREBOGKNILDQEKISLGEQYSPDWLMELFEQT
WGKARTESLGAYFRQNPSLDLRINPLKTSRVEVAQSLAELNITTTAMAGLPQGLRLGG
KTGAITQLPGFAEGWYTVQDASAQWVAQILNPQPEBTIFDVCAAPGGKTTHIAELMGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDVVFCILTFFILGAVGLSRQQAISLDLPRASTGAPQMREMÄNYSLDDLGQLYVEKQP
VSQEGMYSALQNYHQYNPSGLIVLHASRNASYNDVVQLLDTLRTVGGDRVALATLPGD
GQTPSGMNPNSFNNPNLGLPGMTPGNAFPNGANPGMSNFNNSNPGGSGAGVPNFSNTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation="MNPIELMQKGGVAMWPLLLLSILSVSTIIERLWFWGQVILKSSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TASRILDTAARDWDTAIRVAQDSRRFPIAKYLLAPLRLPHPDPEVFHLALESAADDQL
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STAAGLITALVSLAFYRVFQGLWFNQMRVFRRVGSELEVLYRQRWFEEEMAYDDGLTP
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LEVFVNAPLAVCEERDVKGLYAKARSGEIKGFTGIDDPYEPPTNPDVECRTDLEELDE
SVGKIWQKLVDLKYIEG"
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SQIWPINSFNTLEAEVTFQIDINNDDLLGDRLTTVENQGNVSLLEGILGNYYVOSGDD
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SLETAFNQADTSPEFDVRIQNLAFRVDTVIDSTGPVDPIANEIGVVAENGFFFVLLPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LTTPIKYLGEAFDNNLGNWQALAAETVQGVNQVLWQNLDTNQIGVWNSSADWNWISSN
                                                                                                                                                                                                                         PEY I AF SGDGTKAWVTLQENNSVALIDIATTTVEAILPLGFKDHSLPGNGLDASDRDG
                                                                                                                                                                                SIVDITGGFTNLVAQNATFDGFNAQKAELQSAGVRFLGQIFDADGNVVRESTVAEDLE
                                                                                  LDLADPTNPVKIEDLALNFDGIPPGFSPVPNSVAVGKAGTPSAGIVAVSLAIRDDLNN
                                                                                                                            QEAGQVQFFDATTGAFLGKVSVGFLPDMVTFSPDGTKILTANEGEPNESYTVDPVGSV
                                    /translation="MTINSGVSLISKIGGFASSNGAEIPAFDPGTKRLFVVAGDVIEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LPGMPDANGNVSPNPGMNPGFPGGGAMSPDPNSQSPNLPGMGNTVPSAPQQ"
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/db_xref="piD:g1652032"
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/db_xref="PID:91652034"
/transl_table=11
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/db_xref="PID:g1652035"
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/db_xref="PID:g1652033"
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/note="ORF_ID:s1r0678"
/codon_start=1
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/gene="fmu and fmv"
/note="ORF_ID:slr0679"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="ORF_ID:slr0676"
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/transl_table=1
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/product-"alkaline phosphatase"

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/translation="ASLEANVRYMANAMGPEGIRVNGISAGPIRTLAASGIRDFRRML
SHCESVTPLRRTVTTEDVGNTAAFLCSDLSGGITGEIIHVDGGFSIAAMNELELK"
                      Animale e Genetica, Universite di Firenze, Via Romana 17, Florence.
FI 50125, Italy
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MKLYYTPGSCSLSPHIVLRETGLDFSIERIDLRTKKTESGKDFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AINPKGQVPVLQLDNGDILTEGVAIVQYLADLKPDRNLIAPPRALERYHQIEWLNFLA
SEVHKGYSPLFSSDTPESYLPVVKNKLKSKFVYINDVLSKQKCVCGDHFTVADAYLFT
LSOWARPHVALDLTDLSHLQDYLARIAQRPNVHSALVTEGLIKE"
COMPLEMENT (1211..1738)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MGHPEKGCIVPPEVSGVLCEDALPISDIIAPNLLELETLAGGAT
LHNVDQCVKAARQLCQQGPKIVLVKHLSRAGFRHDRFEMLLVTADHSWHYSREVVDFG
ERQPVGVGDLTSGLMLVDLLKGVELKTALEHVAAAVXEVMLKTKEMNEYELQLVAAQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIU32846 10111 bp DNA BCT 27-SEP-1996
Haemophilus influenzae from bases 1805686 to 1815796 (section 161
of 163) of the complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 gtatctotgcaggtccaattcgtaccttagcagcatctggtatcaaagatttccgtaaaa 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 tgitgagccattgcgaatctgtcacccctttacgtcgcacagtcactactgaagatgtgg 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haemophilus influenzae
Eubacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        620 ITCITAAAGAAATCGAAGAGGGTGCACCTITAAAACGTAAACGTTGATCAAGTAGAAGTAG 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190 gtaatactgcagctttcttatgctctgacttatctggcgggatcaccggtgaaatcattc 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           680 GTAAAACAGCGGCTTACTTRTTAAGTGACTTATCAAGTGGCGTTACAGGTGAAAATATTC 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 tagaagcaaacgtacgttatatggcaaatgctatgggtcctgaaggtattcgtgttaacg 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches 95; Indels
                                                                                                                                                                        /note="orfl; similar to E.coli EnvM"
                                                                                                                                                                                                                                                                                                                                                                                               transferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 8.6%; Score 66; DB 25;
Local Similarity 62.5%; Pred. No. 5.34e-29;
Nes 160; Conservative 1; Mismatches 95
                                                                                                         /organism="Proteus mirabilis"
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                                                                                                                                                                                                                                                                                                                                                                                         /product="glutathione tr
/db_xref="PID:g1053076"
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/trans1_table=11
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                                            Italy
Location/Qualifiers
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                                                                                                                                    /strain="AF 2924"
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GLGTLHRNPDLRWRQTPATIATLLPLQQALLKAIAPLVKSGGTLVYSTCTLNPAENEA
QIERFLQDHEDWRSEPFEWTSPQGQTNSVTSGMLTILPHHHQDGFFIANLKKA"
                                                                                                                                                                                                                                                                                                                 Db 102039 tggctcgggggcaaaacccttgatgaccaatggcggtagcatcattaccctgacttact 102098
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Perito, B., Allocati, N., Casalone, E., Masulli, M., Dragani, B.,
Polsinelli, M., Aceto, A. and Di Ilio, C.
Molecular cloning and overexpression of a glutathione transferase
gene from Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (13-OCT-1995) Enrico Casalone, Dipartimento di Biologia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PMU38482 2123 bp DNA BCT 06-SEP-1996
Proteus mirabilis glutathione transferase (gstB) gene, complete
                                                                                                                                                                                                                                                                                                                                                           383 TGGCTCATGAAGCTAAAAAATTAATGCCAGAAGGTGGTAGCATTGTTGCAACAACATATT 442
                                                                                                                                                                                                                                                                                                                                                                                                                                              443 TAGGTGGCGAATTCGCAGTTCAAAATTATAATGTGATGGGTGTTGCTAAAGCGAGCTTAG 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The amino acid sequence of glutathione transferase from Proteus mirabilis, a prototype of a new class of enzymes Eur. J. Blochem. 211 (3), 421-425 (1993)
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Mignogna, G., Allocati, N., Aceto, A., Piccolomini, R., Di Ilio, C.,
Barra, D. and Martini, F.
                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                             /product="hypothetical protein"
                                                                                                                                                                                                                                                               4.50e-47;
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Pred. No. 4.50e-47
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                                                                                                                                                    /db_xref="Pip:g1652036"
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Proteus mirabilis
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/note="ORF_ID:s1r0680"
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les 226; Conservative
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All other authors are with The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD, 20850.
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Submitted (27-SEP-1996) The Institute for Genomic Research, 9712

Medical Center Dr. Rockville, Maryland 20850, USA

The H. influenzae sequence has been updated by R. Fleischmann. New
database matches have been assigned, product names have been
improved, and a number of frame shifts have been corrected. We
gratefully acknowledge the work of Tatusov et. al. We have
incorporated their annotation into the /notes fields of the
Fleischmann, R.D., Adams, M.D., White, O., Clayton, R.A., Kirkness, E.F., Kerlavage, A.R., Bult, C.J., Tomb, J.-F., Dougherty, B.A., Meritck, J.M., McKenney, K., Sutton, G., Fitzhugh, W., Fields, C.A., Gocayne, J.D., Scott, J.D., Shirley, R., Liu, L.-I., Glodek, A., Kelley, J.M., Weidman, J.F., Phillips, C.A., Spriggs, T., Hedblom, E., Cotton, M.D., Utterback, T.R., Hanna, M.C., Nguyen, D.T., Saudek, D.M., Branen, R.C., Fine, L.D., Fritchman, J.L., Fuhrmann, J.L., Geoghagen, N.S.M., Ghehm, C.L., McDonald, L.A., Small, K.V., Fraser, C.M., Smith, H.O. and Venter, J.C.
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Kirkness, E.F., Kerlavage, A.R., Bult, C.J., Tomb, J.-F.,
Dougherty, B.A., Merrick, J.M., McKenney, K., Sutton, G., FitzHugh, W.,
Fields, C.A., Gocayne, J.D., Soott, J.D., Shirley, R., Liu, L.-I.,
Glodek, A., Kelley, J.M., Weidman, J.F., Phillips, C.A., Spriggs, T.,
Hedblom, E., Cotton, M.D., Utterback, T.R., Hanna, M.C., Nguyen, D.T.,
Saudek, D.M., Brandon, R.C., Fine, L.D., Fritchman, J.L.,
Fuhrmann, J.L., Geoghagen, N.S.M., Gnehm, C.L., McDonald, L.A.,
Small, K.V., Fraser, C.M., Smith, H.O. and Venter, J.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L Tatusov.R., Mushegian, A.R., Bork, P., Brown, N.P., Hayes, W.S., Borodovsky, M., Rudd, K.E. and Koonin, E.V.
Metabolism and evolution of haemophilus influenzae deduced from whole-genome comparison with escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (27-JUL-1995) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, Maryland 20850, USA (bases 1 to 10111)
White, O., Clayton, R.A., Kerlavage, A.R. and Fleischmann, R.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hamilton O. Smith is with the Johns Hopkins University School of Medicine, Baltimore, MD, 21205.
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                                                                                                                                                                                                                                                                                                                                                                                                            Science 269 (5223), 496-512 (1995)
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Address all correspondence to:
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ONSTOTGWKLVVAIADPTAYIALDSQIEQEAKORCFTNYLPGFNIPMLPRELSDELCS
LIANBTREABLUCYIETDLAGNITAKPHFVSAYVOSKKLAYNKVSDYLEGADNAMOPE
MPETAOOIHWLHOFTKARIOWRKTHSLPFKERPDYAFVLAENGKVOEIKAETRIANO
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TWYSPIRKYSDWVNHRLIKAVLAKOPYSERPONDYLARLOEARRONRLYERDIADWLYC
RYLADKVASNAFFEARVODVARAGIRVOLLENGASIFIPAATLHNNKEEIQLNPDELA
LYIKGERTYKIGDMYKVKLTEVKEATRSIVGLENGASIFIPAATLHNNKEEIGLNPDELA
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ATVQAINDAGTFVKVQSTEDDIEDSAATKDDNKNQALKAGDTLTLKAGKNLKAKLDQG
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TENVDLYAGYDNWFETTGDKWTLDVVLTAKENGKTTEVKFTPKTSVIKDNNGKLLTGK
OLKDANTGTATNATEDTDEAMA"
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IAPPSMKKVMHGDKIKATIEKQGDKEQAEPEALIEPMLTRFIAKVRFNKDKKLQVLVD
HPSINQPIGAQQAKSVKEELQEGDWVVANLKTHPLRDDRFFYATINQLICRADDELAP
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SIQNCFAELSKRWDKFDGFIHAIAFAPGDQLDGDYVNAATREGYRIAHDISAYSFVAM
AQAARPYLNPNAALLTLSYLGAERAIPNYNVMCLAKASLEAATRVMAADLGKEGIRVN
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AVDSCLMVIDSAKGVEERTIKLMEVTRLRDTPIITFMNKLDRDIRDFIELLDEVENVL
KRAPITWPPIGGKLERGYVHLARDFYLYQSOGGSTIQAVRVYKGLNNPELDSVAVG
DDLAQQLREELELVGAGASNEEDAFIKGELTPVFFGTALGNFGVPFLDLGLTQWAPR
PQSRQADTRTVESAEEKFSGFVFKIQAMMDPKHPDRVPFMRVYSGKYEKGMKLKHYNI
GKDVVISDALTFMAGDRAHAEEAYAGDIIGLHNHGTIQIGDFTFTGFTGIPPRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WWVTLARHEQSRYPVRGAEPYEMLDQKTRENLTALHFVTIDSESTMDMDDALYIEPIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AISAGPIRTLAASGIKNFKKMLSTFEKTAALRRTVTIEDVGNSAAFLCSDLASGITGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MSYPLEEVNKRRTFAIISHPDAGKTTITEKVLLYGNAIQTAGSV
                                                                                                                                                                                                                                                                           /note="similar to SP:003155 percent identity: 28.6; identified by sequence similarity; putative. E. Koonin: weak similarity to AIDA_ECOLI, BLAST score: 88"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            identified by sequence similarity; putative. E. Koonin: homolog of RNB_ECOLI, BLAST score: 529"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to GB:M97219_1 percent identity: 75.3; identified by sequence similarity; putative. E. Koonin: homolog of FABI_ECOLI, BLAST score: 978"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"similar to GB:U14003_286 percent identity: 86.0; identified by sequence similarity; putative. E. Koonin: homolog of RF3_ECOLI, BLAST score: 2387"
search capability are available at TIGR's World Wide Web site
(http://www.tigr.org/tdb/mdb/hidb/hidb.html).
    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="short chain alcohol dehydrogenase homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to SP:P30850 percent identity: 50.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="peptide-chain-release factor 3 (prfC)"
/db_xref="PID:g1574592"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="exoribonuclease II (RNaseII)"
                                                                                                                                                              /organism="Haemophilus influenzae"
                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="adhesin (aidA-I)"
/db_xref="PID:g1574589"
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/gene="H11734"
                                                                                                                                                                                                  complement(1685..2581)
/gene="HI1732"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(2937.,4916)
/gene="H11733"
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PELFRRIRLKDPLKQKQLLKGLVQLSEGGAVQVFRPLLNNDLIVGAVGYLQFDVVVSR
LKTEXNVEAIYENVNVATARWVECADEKKFEEFKRKNEQNLALDGGDNLTYIAPTWVN
                                                                                                                                                                                                                                                                        /translation="MDFNFIEFLGYMATFFVAASFLFKSIVHLRIVNSIGAILFVIYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
/translation="MTLIEQIITIGICIVAVQFTRLLPFFVFPVNRPIPQYIRYLGKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MNLSQQNQHSNPITEAAKATFPYSVPMIAGFLFLGIAYGIYMKA
LGFGFLYPTLMALLIYAGSVEFIAAGALIAPFSPISVLLITLMISARQIFYGISMLEK
YGIHIGKKRWYLITTLVDESFSLNYMAKIPPHLDKGWYMFFVSLYLHIYWVLGAAMGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LPPAMFGMLVVYCYKNIEILTGYHGIPDLLAGIVVLGLHFWKKNMFLSIAVGTLFYMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="H. influenzae predicted coding region HI1737"
/db_xref="PID:g1574595"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="H. influenzae predicted coding region HI1738"
/db_xref="PID:g1574596"
                                                                                                                                                                                        /product="H. influenzae predicted coding region HI1736"
/db_xref="PID:g1574594"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5035 gaaacctgcatcaacgtgaacgatttcgccagtaatgccagaggctaagtcagagcataa 5094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   516 TITAACAITIGCIICTAAGCICGCIIIAGCAACACCCAICACAITATAAITITIGAACIGC 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               756 GAATCCGCTATCTACATGAATATTTTCACCTGTAACGCCACTTGATAAGTCACTTAAYAA 697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="trans-activator of metE and metH (metR)" /db_xref="PID:g1574593"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ttcaaaggtggaaagcattttcttgaagtttttaatgcctgatgcggctagggtgcggat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.3%; Score 56; DB 23; Length 101
58.5%; Pred. No. 1.87e-21;
ttive 1; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                       /gene="H11737"
/note="identified by GeneMark; putative"
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                                                                                                                                  /note="identified by GeneMark; putative"
                                                                                                                                                                                                                                                                                                 LIITAYPVALLNAFLVVVNIYQLWRLKQENLSK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPTLIGIWLILTMRITKLETKLESLK"
complement(9031..9960)
                                                                                  complement(7625..7858)
                                                                                                                                                                                                                                                                                                                                 complement(7961..8290)
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                                                        LNLAQERYPDVVFYKTREH
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tches 186; Conservative
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Submitted (27-SEP-1996) to the EMBL/GenBank/DDBJ databases. The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, Maryland 20850, USA The Influenza sequence has pendated by R. Fleischmann. New database matches have been assigned, product names have been improved, and a number of frame shifts have been corrected. We gratefully acknowledge the work of Tatusov et al. We have incorporated their annotation into the /notes fields of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    I Tatusov R., Mushegian A.R., Bork P., Brown N.P., Hayes W.S.,
Borodovsky M., Rudd K.E., Koonin E.V.;
Metabolism and evolution of haemophilus influenzae deduced from a
whole-genome comparison with escherichia coli";
Curr. Biol. 6:279-291(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fleischmann R.D., Adams M.D., White O., Clayton R.A.,
Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.F.,
Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W.,
Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.I.,
Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T.,
Hedblom E., Cotton M.D., Ofterback T.R., Hanna M.C., Nguyen D.T.,
Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L.,
Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A.,
Small K.V., Fraser C.M., Smith H.O., Venter J.C.,
"Whole-genome random sequencing and assembly of Haemophilus
influenzae Rd",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., FitzHugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.,
                                                                                                   91574588
92-AUG-1995 (Rel. 44, Created)
28-FEB-1997 (Rel. 51, Last updated, Version 8)
Haemophilus influenzae from bases 1805686 to 1815796 (section 161
                                                                                                                                                                                                                                                                                                           Haemophilus influenzae
Eubacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (27-JUL-1995) to the EMBL/GenBank/DDBJ databases.
The Institute for Genomic Research, 9712 Medical Center Dr,
Rockville, Maryland 20850, USA
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                                          standard; DNA; PRO; 10111 BP
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SWISS-PROT; P44300; YH36_HAEIN.
SWISS-PROT; P44301; YH37_HAEIN.
SWISS-PROT; P44432; PABI_HAEIN.
SWISS-PROT; P44440; RNB_HAEIN.
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P45349;
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/translation="MNKIFKVIWNVVTQTWVVVSELTRAHTKRTSATVATAVLATVLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        identified by sequence similarity; putative E. Koonin:
weak similarity to AlDA_ECOLI, BLAST score: 88"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               identified by sequence similarity; putative. E. Koonin: homolog of RNB_ECOLI, BLAST score: 529"
Address all correspondence to: J. Craig Venter The Institute for Genomic Research 9712 Medical Center Dr. Rockville, MD, 20850, USA Hamilton O. Smith is with the Johns Hopkins University School of Medicine, Baltimore, MD, 21205. Joseph M. Merrick is with the State University of New York, Department of Microbiology, Buffalo, NY, 14214. Chris Fields' current address is The National Center for Genome Resources, Sante Fe, NM, 87505. All other authors are with The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD, 20850. Predicted open reading frames were determined using GeneMark software, kindly supplied by Mark Borodovsky, Georgia Institute of Technology, Atlanta, GA, 30332. e-mail:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      percent identity: 28.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to SP:P30850 percent identity: 50.8;
                                                                                                                                                                                                                                                                                               Whiteetigr.org Curation of the genome is ongoing and comments to
the authors are appreciated. Biological role information, putative
                                                                                                                                                                                                                                                                                                                                                     identifications, sequence alignments, on-line name and sequence search capability are available at TIGR's World Wide Web site (http://www.tigr.org/tdb/mdb/hidb/hidb.html).
Loastion/Qualifiers
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complement(1685..2581)
/gene="H11732"
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/db_xref="PID:g1574590"
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/gene="H11733"
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/db_xref="PID:g1574591"
/translation="MRLVFLEILVGFVQRQIFAYTTQVFYANNIGKIMGFLTGKRILV
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                                                                                                                                                                                                               /product="short chain alcohol dehydrogenase homolog (envM)
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                                                             /note="similar to GB:M97219_1 percent identity: 75.3; identified by sequence similarity; putative. E. Koonin: homolog of FABI_ECOLI, BLAST score: 978"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to GB:U14003_286 percent identity: 86.0; identified by sequence similarity; putative. E. Koonin: homolog of RF3_ECOLI, BLAST score: 2387"
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Pred. No. 1.87e-21;
1; Mismatches 131; Indels
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/gene="H11736"
complement(4999..5886)
/gene="HI1734"
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Best Local Similarity 58.5%;
Matches 186; Conservative
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KGRVEEFAAQLGSDJYLQCDVAEDASIDTMRPELGKWPKFDGFVHSIGFAFGDQLDG
BYNAVYREGFRIAHDISSYSFVAMARACRSMLNPGSALLITLSYLGAERAIPWYNWG
LAKASLEANWRXMAMAGPEGYRVNALSAGFIRTLAASGIKDFRKMLAHCEAVTPIRR
TYTIEDVGNSAAFLCSDLSAGISGEVVHVDGGFSIAAMNELELK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ts-phenotype (Ser -> Phe)"
                                                                                                                                                                                                                                      ECUENVM 1366 bp DNA BCT 25-APR-1994 Scherichia coli short chain alcohol dehydrogenase homolog (envM) 977<u>219</u>
                                                                                                                                                                                                                                                                                                                                                                                      Eubacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequences of the envM gene and two mutated alleles in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="change in base causes diazaborine resistance (Gly
                                           5215 tgggcctgcagagattgcattcacacgaataccttctttgcctaaatctgctgccattac 5274
                                                                                                     5275 gcgtgttgcggcttcaagaggcttttgctaggcacattacgttgtagttaggaattgc 5334
 576 TGGACCAGCTGAAATTGCATTAACGCGAATATTATCAGGACCTAAGTCTAATGCTAAATA 517
                                                                                                                            516 TITAACAITIGCITCTAAGCTCGCITTAGCAACACCCAICACATTATAAATITTGAACTGC 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (18-NOV-1992) Helmut Bergler, Institut fuer
Mikrobiologie, Universitaet Graz, Universitaetsplatz 2, Graz,
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Escherichia coli DNA.
Escherichia coli
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/note="partial sequence of boxc"
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336 t
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Pred. No. 4.14e-12;
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Location/Qualifiers
/note="putative"
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254..342
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Best Local Similarity
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/translation="MGFLSGKRILVTGVASKLSIAYGIAQAMHREGAELAFTYQNDKL
VGNAVEREFAGGGSDYTVQCDYAEDASIDTMFRELGKWWFKPGFVHSTGFAFDQDLG
DYNAVTREGFRIAHDISSYSTVAMAKAGRSMLNFGSALLTLSYLGABERAIPNYNWG
LAKASLEANYRYMANAMGPEGVRVNAISAGFIRTLAAAGSIKDFRKMLAHGEAYPPIRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kater,M.M., Koningstein,G.M., Nijkamp,H.J. and Stuitje,A.R.
The use of a hybrid genetic system to study the functional
relationship between prokaryotic and plant multi-enzyme fatty acid
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Eubacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Submitted (08-APR-1994) M.M. Kater, Institute for Molecular
Biological Sciences, Dept of Genetics, BioCentrum Amsterdam, Vri
Universiteit, De Boelelaan 1087, 1081 HV Amsterdam, NETHERLANDS
Location/Qualifiers
                                                                                                                                                                                                                                                                                                            ctggcggcctccggtatcaaagacttccgcaaaatgctggctcattgcgaagccgttacc 1045
                                                                                                                                                                                                                                                                                                                                                                                                                               1046 ccgattcgccgtaccgttactattgaagatgtgggtaactctgcgggcattcctgtgctcc 1105
                                                            866 aactacaacgttatgggtctggcaaaagcgtctctggaagcgaacgtgcgctatatggcg 925
                                                                                                                                                                                  926 aacgcgatgggtccggaaggtgtgcgtgttaacgccatctctgctggtggtccgatccgtact 985
                                                                                                                                                                                                                                                                                                                                                                     586 TTAAGTGCAAAAGGTGTGGGTGGTTTCAATACAATTCTTAAAGAAATCGAAGAGCGTGCA 645
                                                                                                                                                                                                                                            526 TIAGACTIAGGICCIGATAATATICGCGITAATGCAATTICAGCIGGICCAATCCGTACA 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           646 CCTTTAAAACGTAACGTTGATCAAGTAGAAGTAGGTAAAACAGCGGCTTACTTRTTAAGT 705
                                                                                                                      466 AATTATAATGTGATGGGTGTTGCTAAAGCGAGCTTAGAAGCAAATGTTAAATATTTAGCA 525
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      Gaps
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1338..1356
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/clone_lib="Sau3A partial library in pUC19"
/clone="pEN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 706 GACTTATCAAGTGGCGTTACAGGTGAAAATATTCATGTAGATAGCGGATTC
1; Mismatches 124; Indels
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Escherichia coli.
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Plant Mol. Biol. 25 (5), 771-790 (1994)
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/db_xref="PID:9587106"
/db_xref="SWISS-PROT:P29132"
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/organism="Escherichia coli"
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Kater, M.M., Koningst
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166; Conservative
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ORIGIN

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GKSLIAKAICGVNKDNWRYTADRARFDDIDLIRLSARERRKIVGHNVSMIFQEPQSCL
DPSERVGROLAGNIFDAWIYKGRWYORFGWRKRRAIELLHWYGYIKDHKDAMSRPYELT
BECCOKWHIAITALANOPRLLIADEPTNSMEPTTQAOIFRLLTRINGNSNTIILLISHD
LQMLSQWADKINVLYCGGYTVETAPSKELVTWPHHPYTQALIRAIPDFGSAAMPHKSRLN
TLPGAIPLLEQLPIGCRLGFRCPYAQRECIVTPRLTGAKNHLYACHFPLNMEKE"
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FGGWFAPYGIDQQFLGYQLLPPSWSRYGEVSFFLGTDDLGRDVLSRLLSGAAPTVGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MIDKIKSNARDLRRNLTLQERKLWRYLRSRRFSDFKFRRQHPVG
SYILDFACCSARVVVELDGGQHDLAVAYDSRRTSWLESQGWTVLRFWNNEIDCNEETV
LENILQELNRRSPSP"
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PRORISQUILDFPLRAMDIEPEPORRKOIETWRWGGLDPHVYSYPHMIAPGGKQRLG
LARALILRPKVIIDDEALASLDMSKRSQLINLMLELQEKOGISYIYTQHIGMKKHIS
DQVLVMHOGEVVERGSTADVLASPLHELITKRLIAGHFGEALTADAWRKDR"
                                                                                                                                                                                                                                                                                                                                                                                                           KGRVBEERAQUESDIYUQCDYAEDASIDTMENELGKVWPKFDGFVHSIGFAPGDQLDG
KGRVBEERAQUESDIYUQCDYAEDASIDTMENELGKVWPKFDGFVHSIGFAPGDQLDG
DYVNAVTREGFKIAHDISSYSFVAMKACRSMLNPGSALLTLSYLGAERAIPPYNWG
DYVNAVTREGFKIAHDISSYSFVAMKACRSMLNPGSALLTLSYLGAERAIPPYNWG
TARASLEANANNAMGPEGVRVNAISAGPITLAASGIKDFRKMLAHCEAVTPIRR
TVTIEDVGNSAAFLCSDLSAGISGEVVHVDGGFSIAAMNELELK"
complement(2491..2844)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MIETLLEVRNLSKTFRYRTGWFRRQTVEAVKPLSFTLREGQTLA
                                                                                                                                                                                                                                                                                                                                                                              /translation="MGFLSGKRILVTGVASKLSIAYGIAQAMHREGAELAFTYQNDKL
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/db_xref="PID:91787549"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="sapr"
/note="f268; 100 pct identical to SAPF_ECOLI SW: P36637"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="ycjD"
/note="f117; 100 pct identical to YCJD_ECOLI SW: P45736"
                                                                                                                                                                                                                                                                                  /product="enoyl-[acyl-carrier-protein] reductase (NADH)"
/db_xref="PID:91787545"
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SAPD_ECOLI SW: P36635 but has 300 additional N-terminal
residues; 96 pct identical to 330 aa SAPD_SALIY SW:
                                                                                                                                                                                                   /note="f262; 100 pct identical to FABI_ECOLI SW: P29132; CG Site No. 812; alternate name fabI"
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/product="peptide transport system ATP-binding protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="hypothetical 14.0 kD protein in envM-sapF
               /note="corresponds to X78733; (ECENVMACP) 1..1905" complement(1157..2526)
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/note="corresponds to U08190; (ECU08190) 1..1294"
complement(2912..3718)
                                                                                  /note="corresponds to M97219; (ECOENVM) 1..1366" complement(1335..2123)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          intergenic region"
/db_xref="PID:g1787546"
/transl_table=11
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complement(755..2652)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="sapD"
                                                                                                                                                    /gene="fabI'
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LASSPSIIDNRSRQHLNDVGLTAWDCVIISQIIGFTGFQARTIATFQAYLGHPVRULP
ELEDONYADALFADESLRAMESSYEVERLPERHYKSSTABLCQLAEILSLHPISLSLL
EKLLINGYRQPDROLAALLCARINGSPACFATCMDSSNBYKISTLAMKGFNEIN
WADRHSVERATVQAIQWLTRAPDRFSAAQFSPLLEHEKSSTQIINLLWWSGLCGWINR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MLSPIRLSPLPALRQDNDFLYDQGAPMEQRHITGKSHWYHETQS
STTEYDVLPLVPEAAKVSDPFLLDVILEKETLAPFLSWLDPARVLAVDLFPDQLTVTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ECAE000227 10477 bp DNA BCT 21-JAN-1997 Escherichia coli from bases 1346941 to 1357417 (section 117 of 400) of the complete genome.

AE000227 U00096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence was determined as part of the E. coli Genome Project (Frederick R. Blattner, director) at the University of Wisconsin-Madison. Supported by award HG00301 from the NIH Human Genome Project. The entire sequence was independently determined from E. coli MG1655; overlaps with other sequence determinations are annotated.
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hote="fd01" This 401 aa orf is 25 pct identical (7 gaps)
to 166 residues of an approx. 600 aa protein HEXA_ALTSO
SW: P488231; UUG start"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eubacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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                                                                                                                                                                                                             992 aactacaacgttatgggtctggcaaaagcgtctctggaagcgaacgtgcgctatatggcg 1051
                                                                                                                                                                                                                                                                                                                                  1172 ccgattcgccgtaccgttactattgaagatgtgggtaactctgcgggcattcctgtgctcc 1231
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1112 ctggcggcctccggtatcaaagacttccgcaaaatgctggctcattgcgaagccgttacc 1171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   645
                                                                                                                                                                                                                                                                         466 AATTATAATGTGATGGGTGTTGCTAAAGCGAGCTTAGAAGCAAATGTTAAATATTTAGCA 525
                                                                                                                                                                                                                                                                                                                                                                                           526 TIAGACTIAGGICCIGAIAATATICGCGITAATGCAATTICAGCIGGICCAATCCGTACA 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        646 CCTTTAAAACGTAACGTTGATCAAGTAGAAGTAGGTAAAACAGCGGCTTACTTRTTAAGT 705
                                                                                                                                                          Gaps
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Blattner, F.R., Plunkett, G., III, Mayhew, G.F., Perna, N.T and
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                                                                                           Length 1905;
                                                                                                                                                    Mismatches 124; Indels
                                                                                              DB 21; L
4.14e-12;
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         470
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                                                                                              Score 43;
Pred. No.
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         484
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                                                                                        y match
Local Similarity 57.0%;
hes 166; Conservative
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PVEPOKTORTEPTRKANADDVYFTFOR IFDRINDWHINVNGSNFPYFDSLOFADNVKSV
RKLDNHTVEFRLAQPDASFHMILATHYSNWASAFARKLEKEREDRQELDLDROPYGTGFY
GLSETRAGOFIRLOFROPTRORYASSWASAFARKLEKERDRQELDLDROPYGTGFY
GLSILRADDFRKLETLERGMNVAXLARNTAKPPLNALALALALNNGRLMGSIYVG
TARFTAASILLRASWAYDNASATIETNYMPKSREQLAKSGLGENTLKLKUMPTSRGAMNPS
FARTAASILLRASWAYDNASATIETNYMPKSREQLAKSGLGENTLKLKUMPTSRGAMNPS
FARTAASILLRADDAQVOWYVYIVVPVEGREQERALMDMSHBDTLLSGWATDSNDPDSFFRD
LLSCAAIHSOTNLAHWCDPREDSVLEKRALSSGQLAARIEAYDGSNDPDSFFRD
                                                                                                                                                                                                                                                                                                                                                                                     VFWFWGLIHWDFGVSSINGOPIAGOLKEVFPAIMELCILAFGFALITGABLWAW
VFWFWGLIHWDFGVSSINGOPIAGOLKEVFPAIMELCILAFGFALITGIPUGABLWAW
RHKWQDNLINAIALIGFSIPVFWLALLLITECSLTLGWLPVSGRFDLLYGIPUGAIAGIT
LICAMLSDSSWRDEMIMSAIRHMILPVITLGYAPTTEVIRLARISTIEVYDONYVRAA
ATRGLSRFTILRRHVLHWALPVIPRIGLQFSTMLTLAMITEMYFSWPGLGRWLINAI
RQQDYAAISAGVWYGSSLVIYWVISDILGAMANPLKHKEWYALR"
COMPLEMENT (6551..8194)
AMFAVWLALLPRAVRSIYSMVHDELEKEYVIAARLDGASTLNILWFAVMPNITAGLVT
                               EITRALSMAILDIAALGFLDLGAQLPSPEWGAMLGDALELIYVAPWTVMLPGAAIMIS
                                                                                                                                                                                                                                                                                                                                                            /translation="MIIFTLRRILLLIVTLFLLTFVGFSLSYFTPHAPLQGASLWNAW
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complement(8507..8752)
/note="f81; This 81 aa orf is 31 pct identical (2 gaps) to
66 residues of an approx. 872 aa protein RPAL_METH SW:
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FWOLFPPDISRFKDPDAALPEIALYVGGKLEOSIFLCTTFVNTLASGLASHASVSRLI
FWGRDWYPEBVYGYYHEWRPAALNVINVGIVALGALFFDLVTATALINFGALVAF
TFVNLSYFNHFWRRKOHNKSWRDHFHYLLMPLVGALTVGVLWVNLESTSLTLGLVWAS
LGGAYLWYLIRPRKKVPLYDGDRTPVSET"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MNHDIPLKYFDIADEYATECAEPVAEAERTPLAHYFOLLLTRLM
NNEEISEEAOHEMAAEAGINFVRIDEIAEFLNOWGNE"
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SATTYAQKSINPHVGFWYGWSSLLDYLFLPMINVLLAKIYLSALFPEYPPWWYVTFY
AILTRANLKSVNLVANFNTLEVLVQISIMVVFIFLVVQGLHKGBGVGTVWSLQPFISE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MRQVLSSLLVIAGLVSGQAIAAPESPPHADIRDSGFVYCVSGQV
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/db_xref="PID:g1787553"
/transl_table=11
/translation="MISGRHDRRPYYAGEAAIWAINSPINIAAQPGKTRLRKSLKLWQ
                                                                                                                                                                                                                                                                       /product="peptide transport system permease protein SapB"
/db_xref="PID:g1787550"
/transl_table=11
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Anote-"f479; This 479 as orf is 63 pct identical (1 gaps) to 446 residues of an approx. 456 as protein YEEF_ECOLI SW: P33016; UNG start"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="f547; 100 pct identical to GB: ECSAPABCD_1
ACCESSION: x97282; 90 pct identical (2 gaps) to 549 aa
SAPA_SALTY SW: P36634"
                                                                                                                                             /note="f321; 100 pct identical to GB: ECSAPABCD_2
ACCESSION: x97282; 91 pct identical to SAPB_SALIT SW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="peptide transport periplasmic protein SapA
precursor"
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Pred. No. 4.14e-12;
1; Mismatches 124; Indels
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                                                                                              complement(5589..6554)
                                                              VLLVNLLGDGVRRAIIAGVE"
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Best Local Similarity 57.0%;
Matches 166; Conservative
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CDS

CDS

2681

BASE COUNT

ORIGIN

756 GAATCCGCTATCTACATGAATATTTTCACCTGTAACGCCACTTGATAAGTCACTTAAYAA 697

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Submitted (14-DEC-1996) to the DDBJ/EMBL/GenBank databases.
Hirotada Mori, NARA Institute of Science and Technology, Res. & Edu. Center for Genetic Info.; 8916-5 Takayama, Ikoma, Nara 630-01, Japan (E-mail:hmori@gtc.aist-nara.ac.jp, Tel:81-7437-2-5660,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           osmB; pgpB; pyrF; rlbA; rnb, sapD; sapF; yciH; yciM; ycjD. Scherichia coli (strain.K12) DNA, clone_lib:Kohara lambda miniset library clone:Kohara clone #255.

Escherichia coli
Eubacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (Sites)
Alba, H., Baba, T., Fujita, K., Hayashi, K., Honjo, A., Horiuchi, T.,
Ikemoto, K., Inada, T., Isono, S., Itoh, T., Kanai, K.,
Kasai, H., Kashimoto, K., Kim, S., Kimura, S., Kitagawa, M.,
Kitakawa, M., Makino, K., Masuda, S., Miki, T., Mizobuchi, K., Morti, F.,
Salto, M., Sampel, G., Seki, Y., Tagami, H., Takemoto, K., Wada, C.,
The systematic sequencing of the Escherichia coli genome in Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete and shotgun sequencing; MTCY02B10.18C; acnA; fabI, envM;
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Alba,H., Baba,T., Fujita,K., Hayashi,K., Inada,T., Isono,K.,
Itoh,T., Kasai,H., Kashimoto,K., Kimura,S., Kitakawa,M.,
Kitagawa,M., Makino,K., Miki,T., Mizobuchi,K., Mori,H., Mori,T.,
Kitagawa,M., Nakade,S., Nakamura,Y., Nashimoto,H., Nishio,Y.,
Oshima,T., Saito,N., Sampeli,G., Seki,Y., Sivasundaram,S.,
Tagami,H., Takeda,J., Takemoto,K., Takeuchi,Y., Wada,C.,
Tagami,H., Takeda,J., Takemoto,K., Takeuchi,Y., Wada,C.,
A 570-kb DNA Sequence of the Escherichia coli K-12 Genome
Corresponding to the 28.0-40.1 min Region on the Linkage Map
DNA Res. 3, 363-377 (1966)
1431 gaatgccgcagagttacccacatcttcaatagtaacggtacggcgaatcggggtaacggc 1490
                                                                                                                                                              ttcgcaatgagccagcattttgcggaagtctttgataccggaggccgccagagtacggat 1550
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                                                                         696 GTAAGCCGCTGTTTTACCTACTTCTACTTGATCATCATTACGTTTTAAAGGTGCACGCTC 637
                                                                                                                                                                                                                                                                                                                                                                                          576 TGGACCAGCTGAAATTGCATTAACGCGAATATTATCAGGACCTAAGTCTAATGCTAAATA 517
                                                                                                                                                                                                                                        636 TICGAITICITIAAGAATIGIATIGAAACCACCACACCITITIGCACTIAATGIACGGAI 577
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Members: (1995.4 - 1996.3)
Alba, H., Baba, T., Fujita, K., Hayashi, K., Honjo, A.,
Horiuchi, T., Ikemoto, K., Inada, T., Isono, K., Isono, K.,
Itoh, T., Kanal, K., Kasai, H., Kashimoto, K., Kim, S.,
Kimura, S., Kitaqawa, M., Kitakawa, M., Makino, K.,
Masuda, S., Miki, T., Mizobuchi, K., Mori, H., Moromura, K.,
Nakamura, Y., Nashimoto, H., Nishio, Y., Oshima, T., Saito, N.,
Sampei, G., Seki, Y., Tagami, H., Takemoto, K., Wada, C.,
Yamamoto, Y. and Yano, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1611 gogcacgttcgcttccagagacgcttttgccagacccataacgttgtagtt 1661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E.coli genomic DNA, Kohara clone #255(28.8-29.2 min.).
D90766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Japan E.coli genome DNA sequencing project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 17297)
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GAVLTDGSTLGTLGGAAVGGVIGHQVGK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TETVTQPMGVITHLILEGWELMCLRFRIKAAFVLFAILAAAILVGQGVKSWIKDKVQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="Phosphatidylglycerophosphatase B (EC 3.1.3.27)."
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Headed by:
Name: Takahi Horiuchi
Adaress: National Institute of Basic Biology, Okazaki, 444, Japan
E-mail: Kishori@nlbb.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="ORF_ID:0254-5#1; similar to [PIR Accession Number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="yciM"
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initiation site of ThrA (0 min.).; This clone is from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /ps.ce-nORF_ID:0255#3; similar to [SwissProt Accession
Number P18201]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="GTP cyclohydrolase II (EC 3.5.4.25)"
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/transl_table=11
                                                                                                                                                Address: NARA Institute of Science and Technology, Ikoma, 630-01, Japan
E-mail: hmori@gtc.aist-nara.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="Kohara clone #255"
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                                                                                                                                                                                                                                                   The Japan E. coli genome database
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                                                                                                                                                                                                                                                                              http:bsw3.aist-nara.ac.jp.
Location/Qualifiers
1..17297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="acnA"
                                                                                             Information operator:
Name: Hirotada Mori
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FKKVMDAYGHLEGDQLLEDVSLAILSCLEHDQYLARPGGDEFLVLASNTSQSALEAMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation-"msdsnsrlvystetgridepkaapvrpkgdgvvrigrgjsgrkg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product-"Lipoprotein osmB precursor, osmotically inducible"
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Name: Takashi Horiuchi
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                                                                                                                                                                                                                                                                                                                                                                                        /strain="K12"
                                                                                         Information operator:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="acnA"
                                                                                                                      Name: Hirotada Mori
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete and shotgun sequencing; MTCY02B10.18C; acnA; fabI, envM; SomB; pgPB; pyrF; ribA; rnb; sapD; sapF; yciH; yciM; ycjD. Escherichia coli (strain:K12) DNA, clone_lib:Kohara lambda miniset library clone:Kohara clone #255.
Escherichia coli subacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aiba, H., Baba, T., Fujita, K., Hayashi, K., Honjo, A., Horiuchi, T., Kasai, H., Kashimoto, K., Insono, S., Itoh, T., Kanai, K., Kitakawa, M., Makino, K., Kima, S., Kitakawa, M., Makino, K., Masuda, S., Kitakawa, M., Makino, K., Masuda, S., Miki, T., Mizobuchi, K., Motomura, K., Nakamura, Y., Nashimoto, H., Nishio, Y., Oshima, T., Yamamoto, Y. and Yano, M. Fayes, Seki, Y., Tagami, H., Takemoto, K., Wada, C., The systematic sequencing of the Escherichia coli genome in Japan Ollaboration Information:
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                                                                                                                                                                   12615 gaatgeegeagagttacecaacatetteaatagtaaeggtaeggegaateggggtaaegge 12674
                                                                                                                                                                                                                                                                                                                                                                                   12675 ttcgcaatgagccagcattttgcggaagtctttgataccggaggccgccagagtacggat 12734
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                                                                                                                                                                                                                                                                                                                  696 GTAAGCCGCTGTTTTACCTACTTCTACTTGATCAACGTTACGTTTTAAAGGTGCACGCTC 637
                                                                                                                                                                                                                        756 GAAICCGCIAICIACAIGAAIAITIICACCIGIAACGCCACIIGAIAAGICACIIAAYAA 697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             576 IGGACCAGCTGAAATTGCATTAACGCGAATATTATCAGGACCTAAGTCTAATGCTAAATA 517
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Members: (1995.4 - 1996.3)
Alba'H., Baba'T., Fujita'K., Hayashi,K., Honjo,A.,
Horiuchi,T., Ikemoto,K., Indaa'T., Isono,K., Isono, K., Isono, K., Isono, K., Isono, K., Isono, K., Isono, K., Kim,S.,
Kimura,S., Kitagawa,M., Kitakawa,M., Makino,K.,
Masuda,S., Miki,T., Mizobuchi,K., Mori,H., Motomura,K.,
Sampei,G., Seki,Y., Tagami,H., Nishio,Y., Oshima,T., Saito,N.,
Yamamoto,Y. and Yano,M.
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                                                                         DB 106; Length 17297;
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E.coli genomic DNA, Kohara clone #255(28.8-29.2 min.).
D90766
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                                                                                                                              Indels
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                                                                                                                   1; Mismatches 124;
                                                                                               Pred. No. 4.14e-12;
                                                                         Score 43;
Note: remainder of annotations omitted.
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                                                                Ouery Match 5.6%;
Best Local Similarity 57.0%;
Matches 166; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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KEYWORDS

SOURCE

TITLE COMMENT

RESULT

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AGSIKPDSPAGRYLQGRGVERNDENSYGSRRONEYDDINGALLERALDSYLLDISY
MTRILDDSNVSIYDAAMRYRQEGYPLAVIAGKEYGSGSSRDWAAKGPRLLGIRVVIA
ESFERIHRSNLIGMGILPLEFPOGYTRKTLGLTGERKIDIGDLQNLQPGATVPVTLTR
AGSGGVVPCRCRIDTATELTYYQNDGILHYVIRNMLK"
complement (835..1425)
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PVLARYHSECLTGDALFSLRCDCGFQLEAALTQIAEEGRGILLYHROEGRNIGLLNKI
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AGINIVERYPLIVGRNPNNEHYLDTKAEKMGHLLNK"
Address: National Institute of Basic Biology, Okazaki, 444, Japan
E-mail: Kishori@nibb.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="DSTYIRLSPFFDEMQATPAPVEDIHGARILAMLGDSVTTDHISP
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SGHTWFAASWALLAVGLLWPRRTITIAILLVWATGYMGSRLLIGMHWPRDLVVATLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="Phosphatidy1glycerophosphatase B (EC 3.1.3.27)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Nucleotide position 1340563-1357859 from the initiation site of ThrA (0 min.).; This clone is from Kohara lambda miniset library" /clone="Kohara clone #255" /clone="Kohara clone #255" /clone="Kohara lambda miniset library" /map="28.8 min"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="ORF_ID:0255#2; similar to [PIR Accession Number
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Number P18201]"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
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/db_xref="PID:g1742090"
                                                                                                                               Address: NARA Institute of Science and Technology, Ikoma, 630-01, Japan
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                                                                                                                                                                                                                                                                                                                                                                                             /organism="Escherichia coli"
                                                                                                                                                                 Ikoma, 630-01, Japan
E-mail: hmori@gtc.aist-nara.ac.jp
                                                                                                                                                                                                                                                              coli genome database
                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1..17297
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Submitted (14-DEC-1996) to the DDBJ/EMBL/GenBank databases.
Hirotada Mori, NARA Institute of Science and Technology, Res. &
Adu. Center for Genetic Info.; 8916-5 Takayama, Ikoma, Nara 630-01,
Japan (E-mail:hmori@gtc.aist-nara.ac.jp, Tel:81-7437-2-5660,
Fax:81-7437-2-5669)
                                                                                                                                                                                                                                                                        /translation="MFQDNPLLAQLKQQLHSQTPRAEGVVKATEKGFGFLEVDAQKSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sapb; sapF; ycjC; ycjD.
Escherichia coli (strain:K12) DNA, clone_lib:Kohara lambda miniset
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The systematic sequencing of the Escherichia coli genome in Japan Unpublished (1996)
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Eubacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                    II (EC 3.1.13.1) (Ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12555 gaaaccgccgtcaacgtggaccacttcaccggagataccggcagagagatcggagcacag 12614
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                  /gene="rnb"
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Number P30850]"
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E.coli genomic DNA, Kohara clone #256(29.0-29.4 min.).
D90767
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                                                                                                                                                    /product="Exoribonuclease
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complement(9247..11181)
                                                                                                                                                                                   II) (RNase II)."
/db_xref="PID:q1742100"
                                                                                                                                                                                                                                                                                                                                                                                                Score 43;
                                                                                                                                                                                                                                                                                                                                                                                             y Match 5.6%; Score 43; Local Similarity 57.0%; Pred. No. hes 166; Conservative 1; Mism?
                                                                                                                                                                                                                                                                                                                        Note: remainder of annotations omitted.
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1 (bases 1 to 17769)
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Aiba, H., Ba
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AUTHORS
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   CDS
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FKKVNDAYGHLFGDQLLRDVSLAILSCLEHDQVLARPGGDEFLVLASNTSQSALEAMA
                                                                                                                                                                             MMGRVFMAKGEYAKĀVESLQRVISQDRELVSETLEMLĢTCYQQLGKTAEWAEFLQRAV
EENTGADAELMLADIIEARDGSEAAQVYITRQLQRHPTWRVFHKLMDYHLNEAEEGRA
KESLMVLRDMVGEKVRSKPRYRCQKCGFTAYTLYWHCPSCRAWSTIKPIRGLDGL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VGKEMFTLFCPQFVRELQQRGFDIFLDLKFHDIPNTAAHAVAAAADLGVWNVNVHASG
SARMTAARSLVPFGKDDAFLLIAVYVLSMEASDLVDLGMTLSPADYARRLAALTQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="mSDSNSRLVYSTETGRIDEPKAAPVRPKGDGVVRIQRQTSGRKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MLGGVYQKKSESMVGPLTRQCIQQVHFSKAFIGIDGWQPETGFT
GRDMMRTDVVNAVLEKECEAIVLTDSSKFGAVHSYSIGPVERFNRVITDSKIRASDLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation="MKTVRESTTLYNFLGSHNPYWRLTESSDVLRFSTTETTEPDRTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="Putative aga operon transcriptional repressor." /db_xref="PID:g1742098"
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Number Q11024]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note-"ORF_ID:0255#8; similar to [PIR Accession Number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAVLTDGSTLGTLGGAAVGGVIGHQVGK"
complement (5863..6213)
/notte="ORF_ID:o255#9; similar to [SwissProt Accession
Number P42902]"
                                                                                                                                                                                                                                                                                                                                 /note="ORF_ID:0255#6; similar to [SwissProt Accession Number P08244]"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="PID:91742096"
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/gene="MTCY02B10.18C"
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                                                                                                                                                                                                                                                                                                     /gene="pyrF"
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CLASEQARIREMATYTESTILYNEIGSHNDYWRLTESSDVLRFSTTETTEDDRTL
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SKINDDRAGHLFODQLABOVSLALICSCHENOVTARREGGEFLVLASWTSGSALEAN
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STANDANTASKOLLADDTNLRKALENDQLVIHYQPKITWRGSVRSLEALVRNGSPER
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SSLSQLARFPIDAIKLDQVFVRDIHKQPVSQSLVRAIVAVAQALNLQVIAEGVESAKE
DAFLTKNGINERQGFLFAKPMPAVAFERWYKRYLKRA"
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GENERALI (5914. . 6699)

/ Gene " fabl, , env "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="ORF_ID:0255#12; similar to [SwissProt Accession Number Q11024]"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Nucleotide position 1347168-1364936 from the initiation site of ThrA (0 min.).; This clone is from Kohara lambda miniset library" /clone="Kohara clone #256" /clone="Kohara lambda miniset library" /map="29.0 min" |
Members: (1995.4 - 1996.3)
Alba, H., Baba, T., Fujita, K., Hayashi, K., Honjo, A.,
Alba, H., Isemcro, K., Inada, T., Isono, K., Isono, S.,
Itch, T., Kanai, K., Kasai, H., Kashimoto, K., Kim, S.,
Kimura, S., Kitagawa, M., Kitakawa, M., Makino, K.,
Masuda, S., Miki, T., Mizobuchi, K., Mori, H., Motomura, K.,
Sampei, G., Seki, Y., Taqami, H., Takemoto, K., Wada, C.,
Manamoto, Y. and Yano, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Address: NARA Institute of Science and Technology, Ikoma, 630-01, Japan E-mail: hmori@gtc.aist-nara.ac.jp
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/gene="rnb"
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http:bsw3.aist-nara.ac.jp.
Location/Qualifiers
1..17769
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                                                                                                                                                                                                                                                                                                                                                                                                             Name: Takashi Horiuchi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name: Hirotada Mori
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IIGENGSGKSTLAKMLAGMIEPTSGELLIDDHPLHFGDYSFRSQRIRMIFQDFSTSLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation-"MIDKIKSNARDLRRNLTLQERKLWRYLRSRRFSDFKFRRQHPVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKSLIAKAICGVNKDNWRVTADRMRFDDIDLLRLSARERRKLYGHNYSMIFQEDQSCL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FGGWFAPYGIDQQFLGYQLLPPSWSRYGEVSFFLGTDDLGROYLSKLLSGAAFTVGGA
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AMFAVWLALLPRWVRSIYSMVHDELEKEYVIAARLDGASTLNILWFAVMPNITAGLYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MIETLLEVRNLSKTFRYRTGWFRRQTVEAVKPLSFTLREGQTLA
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Complement(9291..10181)
//note="ORE_ID:0255#20; similar to [SwissProt Accession
Number P36669]"
/codon_start.
/note="ORF_ID:0255#16; similar to [SwissProt Accession Number P29132]; Author-given protein sequence is in conflict with the conceptual translation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           //incte="feet" D:0255#17; similar to [SwissProt Accession Number P45736]"
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/note="ORF_ID:0255#18; similar to [SwissProt Accession
Number P36637]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="Peptide transport system ATP-binding protein
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/note="ORF_ID:257#1; similar to [SwissProt Accession
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                                                                                                                                          /product="Enoyl-[acyl-carrier-protein] reductase (1
(EC 1.3.1.9) (NADH- dependent enoyl-ACP reductase)
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                                                                                                                                                                                                                                                                                                                                                                                                                                     VTIEDVGNSAAFLCSDLSAGISGEVVHVDGGFSIAAMNELELK"
complement(7070..7423)
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/db_xref="PID:g1742111"
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                                                                                                                                                                                                                                         /transli_table=11
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DVFCKTDMFTPTRKMNADDVVFTFQRIFDRNNPWHNVNGSNFPFFDSLQFADNVKSV
DVFCKTDMFTVFFRLAQPDASFLHHLATHYASVMGAFARKLEVERDRQEDCLDRQPVGTGPY
QLSSYRAGQFTRLQPRDFWRGKPLMPQVVDLGSGGTGRLSKLLTGRCDVLAMPAAS
QLSILRDDPRLATIRDPRMVAYLAFVRAPPANNPANSHALALAINNORLMQSIYYG
VFWFNGLIHWDFGVSSINGQPIAEQLKEVFPATMELCILAFGFALIVGIPVGMIAGIT
TENEMODNI.NAIALLGFSIPVFWLALLLTJECSLITGWLPVSGRFDLLYEVKRITGFA
LIDAWLSDSPWRDEMIMSAIRHMILDVITLSVAPTTEVIRLMRISTIEVYDQNYVKAA
ATRGLSRFTILRRHYLHNALPPVIPRIGLOFSTMAITEMVFSWFGLGRWLINAI
RQQDYAAISAGVWVCGSLVIIVNVISDILGAMANPLKHKEWYALR
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Eubacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                    complement(11130.12773)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           756 GAATCCGCTATCTACATGAATATTTTCACCTGTAACGCCACTTGATAAGTCACTTAAYAA 697
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Pred. No. 4.14e-12;
1; Mismatches 124; Indels 0;
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Turnowsky,F., Fuchs,K., Jeschek,C. and Hoegenauer,G.
envM genes of Salmonella typhimurium and Escherichia
J. Bacteriol. 171, 6555-6565 (1989)
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259..558
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Best Local Similarity 57.0%;
Matches 166; Conservative
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AUTHORS
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/translation="MGFLSGKRILVTGVASKLSIAYGIAQAMHREGAELAFTYONDKL
KGRVEDEFAAQLGSSTVLPCDVAEDASIDAMFRELGNVWPKFDGFVHSTGFAPGDQLDG
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LAKASLEANVRYMAMGPEGVRVNAISAGFIRTLAASGIKDFRKMLAHCEAVTPIRR
TVIIEDVGNSAAFLCSDLSAGISGEVVHVDGGFSIAAMNELELK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene, partial
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"A proposed superfamily of transpoases genes: transposon-like elements in ciliated protezoa and a common 'D35E' motif"; Proc. Natl. Acad. Sci. U.S.A. 91:942-946(1994).
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                                                                                                                                                                                                                                                                                                                                                     Length 1656;
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hypotrichs; Stichotrichida; Oxytrichidae; Oxytricha
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13-WAR-1997 (Rel. 51, Last updated, Version 1)
Oxytricha fallax 57kD zinc finger/protein chimera
                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 4.69e-10;
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                                                                              /db_xref="PID:g153955"
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                          /note="envM protein"
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                                                    /codon_start=1
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1 Similarity 56.0%;
178; Conservative
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676..1464
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Submitted (11-FEB-1997) to the EMBL/GenBank/DDBJ databases.

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/organism="Mycoplasma bovine group
/strain="R2222"
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                                                                                                                                                                                                                              Score 30; DB 111;
Pred. No. 1.26e-03;
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Mycoplasma bovine group 7 gene sequence.
M96587
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                                                                                                                                                                       41 g
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                                            /codon_start=1
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Matches 38: Concerning
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Best Local Similarity 72.2%;
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/translation="HTRDLXKHLLKAHKKXXEXEXXXXLKXLXKRRAREXXXXXXXX
                                                                                                                                                                                                                                                                                                               AXEXXXVXXXRNXLXSEXTKIMIKIQYKKIPVLAQIDLDTSLQSYLILEDSFDKKVIX
                                                                                                                                            /note="this is a bulk sequence that was generated from a PCR product that represents many transposon templates"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transposon="rBBI"
/note="this is a bulk sequence that was generated from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 354)
Witherspoon, D.J., Doak, T.G., Williams, K., Seger, J. and Herrick, G. Selection on the protein-coding genes of the TBE1 family of transposable elements in the ciliates Oxytricha fallax and O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oppublisher

3 (bases I to 354)

Doak,T.G., Williams,K., Witherspoon,D.J. and Herrick,G.

Direct Submission

Submitted (11-FEB-1997) Oncological Science, University of Utah,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OFU89259 354 bp DNA IN-1997 OXYLICha fallax 57kD zinc finger/protein chimera gene, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 arrakhawgamrhwsarytraagytdctcaahaaaagaaargcdagrgaryhhyhdwarg 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 wbgydgwgcyykaayaagcwagmgarwyaswrtrygtaargawdkeregeaaeewvytrr 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryotae; mitochondrial eukaryotes; Alveolata; Ciliophora; hypotrichs; Stichotrichida; Oxytricha.

1 (bases 1 to 354)

Doak T.G., Doerder, F.P., Jahn, C.L. and Herrick, G. A proposed superfamily of transposase genes: transposon-like elements in ciliated protozoa and a common 'D35E' motif Proc. Natl. Acad. Sci. U.S.A. 91 (3), 942-946 (1994)
Oncological Science, University of Utah, School of Med. Rm5C334, USA, UT 84132, USA
                                                                                                                                                                                                   /codon_start=1
/product="57kD zinc finger/protein chimera"
/transl_table=6
                                                                                                                                                                                                                                                                                                                                                                                                                                            49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           Length 354;
                                                                                                                                                                                                                                                                                                                                                                   Sequence 354 BP; 106 A; 42 C; 41 G; 54 T; 111 other;
                                                                                                                                                                                                                                                                                                                                                                                                         Score 30; DB 8; Loured. No. 1.26e~03; 53; Mismatches 49
                                                                                      /organism="Oxytricha fallax"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Oxytricha fallax"/strain="9D1"
                                  Location/Qualifiers
                                                                                                                           /transposon="TBE1"
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Best Local Similarity 26.8%;
Matches 38; Conservative
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Oxytricha fallax
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Mycoplasma bovine group 7 (strain R2222) DNA.
Mycoplasma bovine group 7
Eubacteria; Firmicutes; Low G+C gram-positive bacteria; Mycoplasmas and walled relatives; Mycoplasmatales; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Taylor,T.K., Bashiruddin,J.B. and Gould,A.R. Relationships between members of the Mycoplasma mycoides Cluster as shown by DNA probes and sequence analysis int.J. Syst. Bacteriol. 42, 593-601 (1992)
                                                                                                                                                                                                                                                               1;
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PCR product that represents many transposon templates"
<1..>354
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                                                                                                                                                                    111 others
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Pred. No. 1.26e-03;
0; Mismatches 21; Indels
                                                                                                                                                                                                                                                           53; Mismatches 49; Indels
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1 ATGTTAAATCTTGAAAACAA.........GATTCCACGCAATTAAATAA 771 TACAATTTAGAACTTTTGTT.........CTAAGGTGCGTTAATTATT
                                                                                                                         BST-STG-TTP9

100:ESTIO0 101:ESTIO1 102:ESTI02 103:ESTI03 104:ESTI04 100:ESTI00 101:ESTI01 102:ESTI02 103:ESTI03 104:ESTI04 100:ESTI00 101:ESTI01 102:ESTI06 107:ESTI07 108:ESTI08 109:ESTI09 110:ESTI11 112:ESTI12 113:ESTI13 114:ESTI14 115:ESTI12 113:ESTI13 114:ESTI14 115:ESTI12 113:ESTI13 114:ESTI14 115:ESTI12 123:ESTI23 124:ESTI13 125:ESTI23 123:ESTI23 123:ESTI23 123:ESTI23 123:ESTI23 123:ESTI23 123:ESTI23 123:ESTI23 123:ESTI23 123:ESTI23 123:ESTI24 123:ESTI34 123:ESTI24 123:ESTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  n.a. - n.a. database search, using Smith-Waterman algorithm
                                                                                                                                                                                                                                                                 Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             707517 seqs, 256659390 bases x 2
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(1-771) from US08790043A.seq
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175:EST175 176:EST176 177:EST177 178:EST178 179:EST179 180:EST180 181:EST181 182:EST182 183:EST183 184:EST184 185:EST185 186:EST185 187:EST185 187:EST185 187:EST189 190:EST190 191:EST190 191:EST195 196:EST195 ```

Statistics: Mean 10.574; Variance 2.087; scale 5.067

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|           |                       |                                       | C                          | -04          | 04                | -04                 | -04                | -04              | -04                | 03               | 03            | -03            | 503            | 500               | 200              | <b>&gt;</b> C  | ) C          | 0               |         | $\sim$                                                                                | $\mathbf{\circ}$ | $\circ$   |           |            | _ \       |          | 5 8        | -03                | 03       |         | 9     | 20.5 | י כ          | 20-0  | o,         | -01       |            |           |     | -01         | e-01       |                   | e-01               |   |
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|           | red.                  | 400                                   | 3.496                      | O            | 54e-              | .54e                | .54e               | .54e             | 5.54e              | 94e-             | .94e-         | 7.94e          | .94e-          | . 94e-            | -94e             | 040            | 946          | 946-            | .94e-   | .94e-                                                                                 | .94e-            |           | .94e-     | 46.        | a) (      | . L      | 946        | 7.94               | 94e      | ÷.      | 7.946 | 946  | . 746<br>0 4 |       | 01e        | .01e      | .01e       | 010       | 010 | 01e         | 1.01       | 1e                | 6.                 |   |
|           | scription             | 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | ANIMONATOR TO STATE OF THE | Fetal heart, | T84470 Homo sapie | mq88b09.rl Stratage | d21e07.rl Soares f | d39all.rl Soares | a08d07.rl Soares m | 88g01.s1 Homo sa | 07.rl Homo sa | 19883.seq.F Fe | an fetal brain | an aorta cDNA 5'- | alz.sl Homo sapi | NOV. IL HOMO S | aorta conA o | SOA TI HOMO SAT | hrain c | Ношо                                                                                  | Homo sap         | omo sapie | Homo sapi | 1 Soares m | Homo sapi | Homo sap | HOMO SAPLE | 1 Stratage         | Homo sap | o none. | 1 Soa | HOMO | Homo saple   | 1 000 | Apartaar C | HORE OFFI | HOLE       | HOMO SADI |     | cinus comm  | 1 Soares s | e cDNA, partial s | 1198 Arabidopsis t |   |
| SUMMARIES | ΙD                    | 1 0                                   | 000                        |              | 112               | AA13                | 7951               |                  |                    | H85028           | 4720          | $\sim$         | 33B0           | UM238E03          | 4486             | 954            | HUM322D12B   | 9               | 0000    | 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2                                               | 1 (7)            | 2         | 7         | 83         | 9         |          | 4.4        | 1/1502<br>AA157291 | 4        | 82      | 92    | œ    | 0,           | 112   | 7C011      | # C       | 4 T        | 2 0       | 0 0 | 0 00        | 460        | RICS10918A        | 0                  |   |
|           | DB                    | 1 0                                   | 0 1                        | ٦.           | 1 6               | 000                 | . ~                | 17               | 11                 | 72               | Н             | Н              | 4              | 4                 | (A               | ┌,             | 27 I         | - "             | , <     |                                                                                       |                  | _         | 72        | ٠,         |           | 8        |            |                    |          | 16      | ٠.    | _    | 27           | 7,    | <b>⊣</b> ( | 4 L       | <b>~</b> 0 | 0 0       | ז ע | <b>~</b> LC | ے ر        | 23                | Н                  |   |
|           | Length                | 1 6                                   | 200                        | 400          | 249               | 424                 | 435                | 516              | 604                | 132              | 172           | 210            | 214            | 233               | 284              | 294            | 313          | 333             | 000     | 386                                                                                   | 388              | 391       | 398       | 409        | 423       | 432      | 433        | 4 4 6              | 440      | 448     | 450   | 468  | 504          | 200   | 236        | 107       | 207        | 100       | 200 | 4 4         | 4.04       | 491               | 533                |   |
| ð         | s<br>Query<br>Match I | 10                                    | 0.0                        | , c          | 90                | 0                   | 5 6                | 2.9              | 5.9                | 2.7              | 2.7           | 2.7            | 2.7            | 2.7               | 2.7              | 2.7            | 2.7          | - 1             | , (     |                                                                                       | 2.7              | 2.7       | 2.7       | 2.7        | 2.7       | 2.7      | 7.1        | ,,                 |          | 2.7     | 2.7   | 2.7  | 2.7          | 2.7   | 9 10       | 7.0       | 9.0        | 7.0       | 9.7 | 2 ,         | , ,        | 2.6               | 7.6                | I |
|           | Score                 | 1 0                                   | 57                         | 2.0          | 7 (               | 27                  | 2 2 2              | 22               | 22                 | 21               | 21            | 21             | 21             | 21                | 21               | 21             | 21           | 27              | 7,0     | 217                                                                                   | 77               | 21        | 21        | 21         | 21        | 21       | 21         | 77.5               | 217      | 21      | 21    | 21   | 21           | 21    | 500        | 0 0       | 20         | 070       | 070 | 200         | 0 0        | 200               | 20                 | i |
|           | Result<br>No.         |                                       |                            | 7 (          | n <del>-</del>    | <b>+</b> ư          | n w                | 7                | . ۵۵               |                  | -             | c 11           | ٦              | 13                | 14               | 15             | c 16         | 17              | ٠,٠     | 0<br>50<br>60<br>60<br>60<br>60<br>60<br>60<br>60<br>60<br>60<br>60<br>60<br>60<br>60 | 2,0              | 75        | c 23      | •          | 25        | c 26     | 27         | 288                | • •      | 31      |       | 33   | c 34         |       | 36         |           | 38         |           |     |             | 4.4        | 4.0               | 45                 |   |

## ALIGNMENTS

| RESULT 1  |                                                    |
|-----------|----------------------------------------------------|
|           | R95589 337 bp mRNA EST 06-SEP-1995                 |
| LTION     | SMNHADA016014T3 Schistosoma mansoni cDNA 5'.       |
| ACCESSION | R95589                                             |
| NID       | 9975959                                            |
| KEYWORDS  | BST.                                               |
| SOURCE    | blood fluke primer-T3 library-SmAW strain-Egyptian |

```
vector=Bluescript host-Golden Hamster Rsitel=EcoRI Rsite2=XhoI Total mRNA was isolated from adult worms using the acid guanidine thiocyanate method (Chomczynski and Sacchi, 1987). Poly (A)+ RNA was purified by affinity chromatography on Oligo dr Column (Aviv the Lambda zap cDNA cloning system (Stratagene-[Uni-Zap XR Glyapack II cloning kit). The library was constructed using Glyapack II cloning kit). The library was amplified (end titre-0.5 probes (Chorion and tropomyosin genes). The size range of inserts for the library was 0.5Kb - 2.5 KD, the cDNA being directionally phagemid. Bluescript phagemid the XhoI sites of the Bluescript phagemid was excised by mass in vivo excision of the library and inserted into E.coli XLI Blue. The plasmid was purified using the Qiagen Qiawell 8 system and sequenced with Tag library was prepared by Hanan Aboel Hamed, Ain Shams Univ., Cairo cairn
 0;
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Platyhelminthes;
Trematoda; Digenea; Strigeidida; Schistosomatoidea;
Schistosomatidae; Schistosoma.
1 (bases 1 to 337)
 2k39d04.rl Soares pregnant uterus NbHPU Homo sapiens cDNA clone AA039422
 Gaps
 Eukaryotze; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 439)
Hillier, L. Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Huthan, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
 Contact: Ridgers, I.L.
Experimental Taxonomy Unit, Zoology
The Natural History Museum
Cromwell Road, South Kensington, London, SW7 5BD, U.K.
Tel: 01719389297
Fax: 01719388754
Email: I.Ridgers@nhm.ac.uk
 ;
0
 Length 337;
 Score 23; DB 76; Length 55;
Pred. No. 3.49e-05;
....matches 8; Indels
 17 others
 Email: T.Ridgers@nbm.ac.uk
Schistosoma mansoni cDNA clone SMNHADA016014T3.
Location/Qualifiers
 /organism="Schistosoma mansoni"
 121 t
 315 CITITCTGAAACTTCACGTGAAGGCTTCTTGTTA 348
 208 ctttnctnaaacttccaatgnnggnttcttgtta 241
 56 g
 /strain="Egyptian"
 The Washu-Merck EST Project
 Contact: Wilson RK
WashU-Merck EST Project
 Match 3.0%;
Local Similarity 76.5%;
 Schistosoma mansoni
 28
C
 Unpublished (1995)
 26; Conservative
 <1..>337
 Unpublished (1995)
 Homo sapiens
 human.
 Query Match
 source
 ORGANISM
 AUTHORS
JOURNAL
 DEFINITION
 BASE COUNT
 ORGANISM
 ERENCE
 Matches
 mRNA
 ACCESSION
 FEATURES
 REFERENCE
 AUTHORS
 KEYWORDS
 COMMENT
 ORIGIN
 TITLE
 COMMENT
 RESULT
 SOURCE
```

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Actional Action of the state of the soft the so
 /Organism="Homo sapiens"
//Organism="Homo sapiens"
//Organism="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2: Mol; mRNA was purified from human fetal hearts (8-10 weeks). CDNA was synthesized using a Mnoi-Oligo dr adaptor-primer. EcoRI adaptors were ligated, followed by digestion with XhoI, for directional cloning into predigested lambda ZAP Express."
 /note="Organ: uterus; Vector: pT713-Pac; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I oligo(dT) primer [5'
 Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28MJ3 rev2 from Amersham
High quality sequence stop: 246.
 N86668 179 bp mRNA EST 01-APR-1996
J9617F Fetal heart, Lambda ZAP Express Homo sapiens cDNA clone
J9617 5' similar to CAVEOLIN.
 0; Gaps
 Molecular Cardiology
University of Toronto
Banting Institute, 100 College St., Toronto, Ontario, M5G1L5
Tel: 4169788758
Fax: 4169785650
Email: 11ewcceutcc.utoronto.ca
 Homo sapiens
Bukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 234 tttggtgcctgtaaagttttacttctattagctgtttcattgctttgcactta 286
 Match 3.0%; Score 23; DB 159; Length 439; Local Similarity 71.7%; Pred. No. 3.49e-05; les 38; Conservative 0; Mismatches 15; Indels
 0; Mismatches 15; Indels
 145 t
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 79 g
 cDNAs from fetal heart (1996)
 /dev_stage="adult"
/lab_host="DH10B"
 Location/Qualifiers
 /sex="female"
 /clone="J9617"
 (bases 1 to 179)
 81 c
 Tel: 314 286 1800
Fax: 314 286 1810
 Unpublished (1996)
 <1..>439
 Contact: Liew CC
 q1439870
 Liew, C.C.
 N86668
 human.
 Query Match
 source
 MRNA
BASE COUNT
ORIGIN
 m
 DEFINITION
 source
 ORGANISM
 Matches
 TITLE
JOURNAL
 ACCESSION
 AUTHORS
 FEATURES
 REFERENCE
 KEYWORDS
 FEATURES
 RESULT
 COMMENT
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 ò
 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;

Bukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;

Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;

Sarcopterygii; Choanta; Tetrapoda; Amniota; Mammalia; Theria;

Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 249)

Sadams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldher, R.A.,

Bult, C.J., Lee, N., Kirkness, E.F.; Weinstock, K.G., Gocayne, J.D.,

White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W.,

Clayton, R.A., Cline, R.T., Cotton, M.D., Barle-Huqhes, J., Fine, L.D.,

FitzGerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M.,

Kelley, J.M., Kilmek, K.M., Kelley, J.C., Liu, L.T., Marmaros, S.M.,

Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T.,

Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L.,

Saudek, D.M., Shirley, R., Small, K.V., Sprigs, F., Ferrie, A.,

Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Cepeda, M.A.,

Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H.,

Melssner, P.S., Olsen, H., Raymond, L., Well, Y.-F., Wing, J., Xu, C.,

Haseltine, W.A., Flelds, C., Fraser, C.M. and Venter, J.C.

Initial Assessment of Human Gene Diversity and Expression Patterns

Barder, D.S., Sallion Basepairs of CDNA Sequence
 Email: tdbinfoetdb.tigr.org
for clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
(tdbinfoetdb.tigr.org).
 ó
 ô
 41 agctataganaagctattgagagtatctagttaatcagtgcagtagttggaaaccttgct 100
 205 AGCGATGAAGAGGTTATTAATGGTTTTGAGCAAATTGGTAAAGATGTTGGCAATATTGAT 264
 06-SEP-1995
 Gaps
 ;
 ö
/clone_lib="Fetal heart, Lambda ZAP Express"
/lab_host="E. coli XL1-Blue"
<1..>179
 Length 179;
 Length 249;
 666 TCAAGTAGAAGTAGGTAAAACAGCGGCTTACTTRITAAGTGACTTATC 713
 69 tcaagttcaagttgctaatacagcaacacatttatgaattgaattatc 116
 Score 22; DB 81; Length 249
Pred. No. 5.54e-04;
0; Mismatches 26; Indels
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EST84470 Homo sapiens CDNA 5' end similar to None.
 1; Mismatches 13; Indels
 human primer=M13 Reverse library=Human Colon.
 Score 22; DB 142;
Pred. No. 5.54e-04;
 The Institute for Genomic Research 932 Clopper Rd, Gaithersburg, MD 20878 rel: 3018699056
 71 t
 100 t
 /organism="Homo sapiens"
 45 g
 Location/Qualifiers
 g
 Unpublished (1995)
Other_ESTs: THC16399
Contact: Venter, JC
 249 bp
 Query Match 2.9%;
Best Local Similarity 70.8%;
 34; Conservative
 34 c
 27 C
 <1..>249
 Homo sapiens
 Local Similarity
les 46; Conserv
 65 a
 Ø
 T35412
g617510
 T35412
 EST.
 Query Match
 mRNA
BASE COUNT
ORIGIN
 DEFINITION
 BASE COUNT
ORIGIN
 ORGANISM
 mRNA
 Matches
 PURNAL
 Matches
 ACCESSION
 REFERENCE
 AUTHORS
 ORDS
 FEATURES
 TITLE
 ENT
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1 (bases 1 to 424)
Marra.M., Hillier.L., Allen.M., Bowles.M., Dietrich.N., Dubuque,T.,
Geisel,S., Kucaba.T., Lacy.M., Le,M., Martin,J., Morris.M.,
Schellenberg,K., Steptce,M., Tan.F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 mq88b09.rl Stratagene mouse melanoma (#937312) Mus musculus cDNA clone 585785 5' similar to SW:DLDH_MYCGE P47513 LIPOAMIDE
 This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 2d21e07.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone W57951
94364733
 02-DEC-1996
 Gaps
 Washu-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
 ;
0
 Score 22; DB 186; Length 424;
Pred. No. 5.54e-04;
0; Mismatches 5; Indels (
 /lab_host="SOLR (kanamycin resistant)" <1..>424
 Contact: Marra M/Mouse EST Project
 265 ttgtttttggtgaagctacaattttagatcaa 296
 Seq primer: primer name ambiguous
High quality sequence stop: 416.
Location/Qualifiers
 Email: mouseest@watson.wustl.edu
 Waterston, R.
The WashU-HHMI Mouse EST Project
 /dev_stage="M2 cells"
 mRNA
 74 g
 DEHYDROGENASE COMPONENT ; .
 424 bp
 Best_Local Similarity 84.4%;
Matches 27; Conservative
 2.98;
 υ
 Unpublished (1996)
 48
 1..424
101 ggtgtatgtnat 112
 265 GGTGTATATCAT 276
 Mus musculus
 house mouse.
 MGI:360433
 AA138421
 q1700622
 human.
 Query Match
 9
 Ŋ
 DEFINITION
 source
 DEFINITION
 mRNA
BASE COUNT
 ORGANISM
 TITLE
JOURNAL
 ACCESSION
 ACCESSION
 REFERENCE
 AUTHORS
 KEYWORDS
SOURCE
 KEYWORDS
 FEATURES
 RESULT
 ORIGIN
 SOURCE
 RESULT
```

```
Wilson, R.
 91274290
 Wilson, R
 human.
 ω
 source
 mRNA
BASE COUNT
 DEFINITION
 TITLE
JOURNAL
COMMENT
 ORGANISM
 Matches
 ACCESSION
 REFERENCE
 AUTHORS
 FEATURES
 KEYWORDS
 TITLE
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 normalization to a cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung
 Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET
 2d39all.rl Soares fetal heart NbHH19W Homo sapiens cDNA clone W67124 5237614
 Homo saplens
Bukaryotes, mitochondrial eukaryotes; Metazoa; Chordata;
Bukaryotes, mitochondrial eukaryotes; Metazoa; Chordata;
1 (bases 1 to 316)
Hilliafr,L., Clark,N., Dubuque,T., Ellistoo,K., Hawkins,M.,
Holman,M., Hultman,M., Rucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
 1 (bases 1 to 435)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
 1; Gaps
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 pry Match 2.9%; Score 22; DB 170; Length 435; bt Local Similarity 80.0%; Pred. No. 5.54e-04; ches 36; Conservative 0; Mismatches 8; Indels 1
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 301 agtgcaaaatgtattgttg-tttcaatacaaaatttaaagcaatc 344
 /organism="Homo sapiens"
 High quality sequence stop: 338.
Location/Qualifiers
 67 g
 Wilson, K.
The WashU-Merck EST Project
 /clone="341316"
 WashU-Merck EST Project
 84 c
 Contact: Wilson RK
 Unpublished (1995)
 <1..>435
 Homo sapiens
 Wilson, R
 numan.
 7
 source
 DEFINITION
 mRNA
BASE COUNT
ORGANISM
 TITLE
JOURNAL
 ORGANISM
 atches
 REFERENCE
 ACCESSION
 AUTHORS
 REFERENCE
 AUTHORS
 KEYWORDS
 FEATURES
 COMMENT
 RESULT
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**Motevalue Control of the Control of Contro
 W02311 604 bp mRNA EST 18-APR-1996 as 208007.rl Soares melanocyte 2NbHW Homo sapiens cDNA clone 291949 5' similar to SW:UBPR HUMAN P40818 PROBABLE UBIQUIIN
 Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 664
Seq primer: mob.REGA+ET
 311 aagotcaaatotttcacctggatgttttgagggggtaatgatgagactattggatttgagg 370
 176 AAGCGCACTTATATCAAATTGATGTTCAAAGCGATGAAGAGGTTATTAATGGTTTTTGAGC 235
 Eukaryotze mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 60,4).
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
 0; Gaps
 Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Score 22; DB 171; Length 516;
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 /dev_stage="19 weeks"
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 Pred. No. 5.54e-04;
 143 t
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 High quality sequence stop: 344. Location/Qualifiers
 122 g
The WashU-Merck EST Project
 The WashU-Merck EST Project
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 Query Match 2.9%;
Best Local Similarity 64.9%;
 <1..>516
≥ 101 c
 48; Conservative
 Contact: Wilson RK
 Unpublished (1995)
 Tel: 314 286 1800
Fax: 314 286 1810
 NbHL19W."
 Unpublished (1995)
 371 atattcctaatgat 384
 236 AAATTGGTAAAGAT 249
 1..516
 Homo sapiens
 147 a
 JOURNAL
```

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Score 21;
 Location/Qualifiers
 30 g
 Location/Qualifiers
 23 g
 Email: est@watson.wustl.edu
 Putative full length read.
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 /clone="221904"
 Washu-Merck EST Project
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Best Local Similarity 75.0%;
Matches 30; Conservative
 30 C
 15 c
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Fax: 314 286 1810
Unpublished (1995)
 Contact: Wilson RK
 <1..>132
 Homo sapiens
 48 a
 51 a
 Query Match
 10
 BASE COUNT
 DEFINITION
 ORGANISM
 mRNA
BASE COUNT
 JOURNAL
 REFERENCE
 AUTHORS
 ACCESSION
 JOURNAL
 FEATURES
 KEYWORDS
 FEATURES
 TITLE
 COMMENT
 ORIGIN
 RESULT
 SOURCE
 ORIGIN
 ŏ
 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Barcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 132)
1 (bases 1 to 132)
1 Hillier, Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Hultman, M., Rucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Levaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: mob.REGA+ET.
High quality sequence stop: 353.
 14-NOV-1995
 Gaps
 .;
0
 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1810
 Score 22; DB 113; Length 604;
Pred. No. 5.54e-04;
0; Mismatches 10; Indels (
 11 others
 /sex="Male"
/lab_host="DH10B (ampicillin resistant)"
 ys88g01.s1 Homo sapiens cDNA clone 221904 3'. H85028
 /clone_lib="Soares melanocyte 2NbHM"
 458 caagetetttaetgggaenttegtaaenttaggaaaatae 497
 152 t
 126 g
 The WashU-Merck EST Project
 Email: est@watson.wustl.edu
 Contact: Wilson RK
WashU-Merck EST Project
 Query Match 2.9%;
Best Local Similarity 75.0%;
Matches 30; Conservative
 149 C
 Homo sapiens
 Wilson, R
 g1064730
 mRNA
BASE COUNT
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 source
 DEFINITION
 ORGANISM
 REFERENCE
 AUTHORS
 ACCESSION
 WORDS
 TITLE
 FEATURES
 RESULT
 COMMENT
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Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
 human clone=74840 library=Stratagene ovary (#937217)
vector=Bluescript SK host=SOLR cells (kanamycin resistant)
primer=M13RP1 Rsitel=EcoR1 Rsitel=Anol Choned unidIrectionally.
Primer: Oligo dr. Total ovary tissue, normal 49 year old caucasian
female. Average insert size: 0.8 kb; Uni-ZAP XR Vector; 5' adaptor
sequence: 5'-GAATICGGCACGAG-3'; 3' adaptor sequence:
 ö
 Email: estewatson.wustl.edu
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
 High quality sequence stops: 73
Source: INAGE Consortium, LLNL
This clone is available robalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
 Dutheria: Primates; Catarrhini; Hominidae: Homo.

1 (bases 1 to 172)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,

Holman,M., Hultman,M., Rucaba, Lennon,G., Marra,M.,

Parsons,J., Rifkin,L., Rohlfing,T., Ten,F., Trevaskis,E.,

WashUr Merck EST Project

Unpublished (1995)

Other_ESTS: y553q07.s1

Contact: Wilson RK
 08-FEB-1995
 Gaps
 Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810
 0;
 DB 17; Length 172;
 Length 132;
 10; Indels
 yb53g07.rl Homo sapiens cDNA clone 74940 5'.
T47205
g649187
 1 ATGITAAAICIIGAAAACAAAACAIAIGICAICAIGGGAA 40
 52 atgitaaatacigiaataaaaacaigticaaicaiggnaa 91
WashU-Merck EST Project
Washington University School of Medicine
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184 bytotcavacagttaaaaaattaaagccagaacagggta 222
 Otsuka Pharmaceutical Co., Ltd
463-10 kagasuno Kawauchi-cho
Tokushima, Tokushima
 Location/Qualifiers
 Otsuka GEN Research Institute
 54 g
 Location/Qualifiers
 Query Match 2.7%;
Best Local Similarity 42.6%;
 Phone: 0886-65-2888
Fax : 0886-37-1035
 32 C
 Query Match
Best Local Similarity 71.8%;
Matches 28; Conservative
 23; Conservative
 Phone: 0886-65-2888
 Fax : 0886-37-1035
 Tsutomu Fujiwara
 CDNA to mRNA.
 Homo sapiens
 35 a
 9965884
 =
=
::
 Japan
 Japan
 Query Match
 source
 13
 BASE COUNT
 DEFINITION
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 ORGANISM
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 Matches
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JOURNAL
 ACCESSION
 BASE COUNT
 REFERENCE
 AUTHORS
 FEATURES
 KEYWORDS
 TITLE
 COMMENT
 FEATURES
 COMMENT
 ORIGIN
 RESULT
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 ORIGIN
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 AA092855 210 bp mRNA EST 24-OCT-1996
119883.seq.F Fetal heart, Lambda ZAP Express Homo sapiens CDNA 5'.
AA092855
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Anote="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2: XhoI: mRNA was purified from human fetal hearts (8:10 weeks).

weeks). cDNA was synthesized using a XhoI-Oligo dr adaptor. primer. EcoRI adaptors were ligated, followed by predigested lambda ZAP Express."

Alone_lib="Fetal heart, Lambda ZAP Express"

/lab_host="E. coli XII-Blue"
 EST(expressed sequence tag); Human fetal brain; similar to none(May 29,1995).
 ö
 ó
 Gaps
 Molecular Cardiology
University of Toronto
Banting Institute, 100 College St., Toronto, Ontario, M5G1L5
Tel: 4169788758
Fax: 416978550
Email: liewcc@utcc.utoronto.ca
 Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 210)
 Gaps
 26-AUG-1995
 Homo sapiens (library: Clontech human fetal brain polyA+ mRNA (#6535)) cDNA to mRNA.
 ò
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0
 98 tttggtatagttgcttttctgattgatttttttttttcctcgaacttttaaa 148
 193 TITGATATAAGIGGGGTICTGGTIGATITAATIGTICTAATAATITITGAA 143
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Seq primer: 5' GAAATTAACCCTCACTAAAGGG 3'
Location/Qualifiers
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Human fetal brain cDNA 3'-end GEN-003B01.
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 84 tctgaaccaattttctcaaaaccagtaat 112
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CDNAs from fetal heart (1996)
Unpublished (1996)
 39 g
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Local Similarity 86.2%;
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Best Local Similarity 70.6%;
Matches 36; Conservative
 Contact: Liew CC
 Homo sapiens
 91637868
 4960367
 numan.
 D59261
 ery Match
 RESULT 11
 DEFINITION
 ORGANISM
 12
 DEFINITION
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AUTHORS
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 BASE COUNT
 ACCESSION
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 KEYWORDS
 FEATURES
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 AUTHORS
 KEYWORDS
 RESULT
 GIN
 SOURCE
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Сp

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Eukaryotee; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 23)
1 (bases I to 23)
1 (kases I to 23)
1 (kases I to 23)
2 (katagiri, K. Katagiri, T., Kawai, A., Kuga, Y., Nagata, M., Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H., Takaichi, A., Takeda, S., Watanabe, T., Takahashi, E.-I., Hirai, Y., Maekawa, H., Shin, S. and Nakamura, Y.
Choublished (305)
Choublished (1995)
Submitted (30-May-1995) to DDBJ by:
 ö
 ö
Takaichi,A., Takeda,S., Watanabe,T., Takahashi,E.-I., Hirai,Y.,
Maekawa H., Shin,S. and Nakamura,Y.
 Homo sapiens (library: Clontech human aorta polyA+ mRNA (#6572))
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 6 dgsgrggggggttttvtdbyattgadddaddtttdaaarrgtktgnwtgttha 59
 ö
 ö
 Length 214;
 Score 21; DB 48; Length 214;
Pred. No. 7.94e-03;
14; Mismatches 17; Indels
 39 others
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Pred. No. 7.94e-03;
2; Mismatches 9; Indels
 EST
 Unpublished (101)
Unpublished (101)
Unpublished (1995)
Submitted (1995) to DDBJ by:
Tsutomu Fujiwara
Otsuka GEN Research Institute
Otsuka Pharmaceutical Co.,Ltd
463-10 kagasuno kawauchi-cho
 54 t
 HUM238E03B 233 bp mRNA
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 /organism="Homo sapiens"
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UIN

KEYWORDS ACCESSION LOCUS DEFINITION

yg25a12.s1 Homo sapiens

284 bp

mRNA EST CDNA clone 33372 3'

22-MAY-1995

Š

383

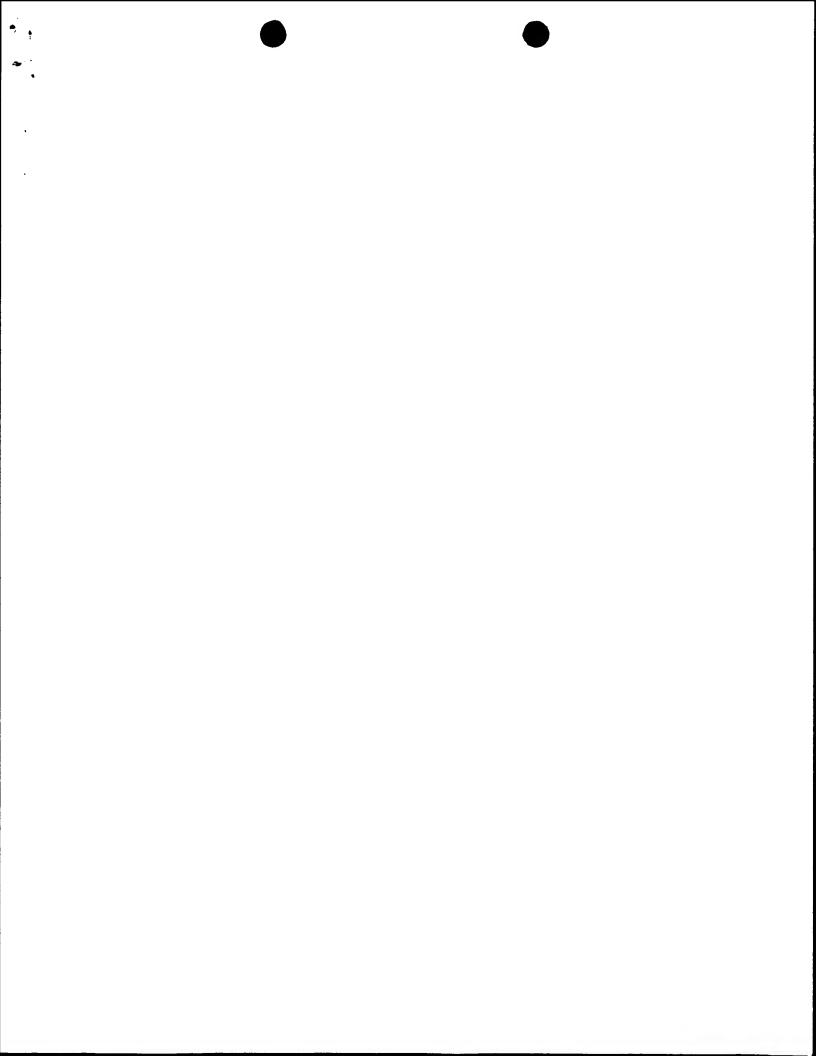
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 SOURCE
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 Query Match
 JOURNAL
 Matches
 AUTHORS
 E COUNT
 RGANISM
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 371
 y Match 2.7%;
Local Similarity 78.4%;
hes 29; Conservative
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
 ye06h07.rl Homo sapiens cDNA clone 116989 5' similar Alu repetitive element;.
 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthy
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
 Homo sapiens
 cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lafmid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima
human clone=116989 library=Soares fetal liver spleen lNFLS vector=pT773D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=ml18RP1 Rsite1=Pac I Rsite2=Eco RI Liver and spleen from a 20 week-post conception male fetus. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5'
 High quality sequence stops: 226 Source: IMAGE Consortium, LLNL
 Tel: 314 286 1800 Fax: 314 286 1810
 Contact: Wilson RK
WashU-Merck EST Project
 Unpublished
 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
 GDB: G00-405-719
 The WashU-Merck EST Project
 Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
 Bonaldo.
 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 Email: est@watson.wustl.edu
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/clone="33372"
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 34 g
 115 t
 8
 Length 284;
 2 others
 Indels
 MO 63108
 23-MAR-1995
 Marra, M.,
 Osteichthyes;
 0,
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ş 망

0

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COMMENT
 Query Match
Best Local Similarity
Thes 24; Conserv
 ORIGIN
 FEATURES
 REFERENCE
 Search completed: Fri Dec
 BASE COUNT
 TITLE
JOURNAL
 AUTHORS
 ORGANISM
 source
 256 taaattagtatgtactcactgtaaaga 282
 99
 TAAATTAGTATTTACTTACCGTAAAGA 125
502 secs
 Contact: Wilson RK
WashUnderck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
Tel: 314 286 1810
Fax: 314 286 1810
 1 (bases 1 to 294)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
 CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.
 Unpublished (1995)
 Homo sapiens
 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 High quality sequence stops: 271
 The WashU-Merck EST Project
 Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Email: est@watson.wustl.edu
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62 c 49 g 8
 Location/Qualifiers
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 5 08:08:05 1997
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 85
 d
 St. Louis, MO
 Length 294;
 Indels
 others
 G., Marra, M.,
 0;
 Gaps
 0
```



Description

DB

Match Length

00

|                                                                     | (WL)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
|---------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Release 2<br>Copyright<br>D                                         | 2.1D John F. Collins, Biocomputing Research Unit.<br>jht (c) 1993, 1994, 1995 University of Edinburgh, U.K.<br>Distribution rights by Intelligenetics, Inc.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| MPsrch_nn n.a.                                                      | . • n.a. database search, using Smith-Waterman algorithm Fri Dec 5 08:08:27 1997; MasPar time 252.09 Seconds not generated.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| Title:<br>Description:<br>Perfect Score:<br>N.A. Sequence:<br>Comp: | >US-08-790-043A-2 (1-771) from US08790043A.seq 771 1 ATGITAAATCITGAAAAGAAGATICCACGCAAITAAAIAA 771 TACAAITIAGAACTITIGITCTAAGGIGCGTIAAITAIT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| Scoring table:                                                      | TABLE default<br>Gap 6                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| Nmatch STD :                                                        | Dbase 0; Query 0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| Searched:                                                           | 359085 seqs, 137405154 bases x 2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| Post-processing:                                                    | Minimum Match 0%<br>Listing first 45 summaries                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| Database:                                                           | BST-STS-THREE  1:EST109 2:EST200 3:EST201 4:EST202 5:EST203 6:EST204  7:EST205 8:EST200 9:EST207 10:EST208 11:EST209 12:EST210  13:EST211 14:EST212 15:EST213 16:EST214 17:EST215  18:EST216 19:EST212 25:EST213 21:EST212 22:EST220  23:EST222 25:EST222 25:EST223 26:EST224 27:EST225  28:EST226 29:EST227 30:EST228 31:EST229 32:EST225  39:EST221 34:EST227 35:EST228 31:EST229 32:EST223  39:EST231 34:EST232 35:EST238 36:ST51 37:STS2 38:STS3  39:STS4 40:STS5 41:ST56 42:ST57 43:ST58 44:ST59 45:ST510  49:GNST11 47:ST51 2 48:ST51 35:EST28 58:GNEST1 65:GNEST1 65:GNEST1 50:GNEST2 51:GNEST3 52:GNEST1 65:GNEST1 50:GNEST1 50:GNEST2 50: |
| Statistics:                                                         | Mean 10.599; Variance 2.102; scale 5.042                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |

2.118e-05
3.39e-04
3.39e-04
3.39e-04
4.77e-03
4.

AA205935 AA088037 DM96D10S G19638 HS1166217 AA251371 G10965 G22403 W84913 W84913 W84913 WA3086 AA019095 AA230876 WAA30876 G21132

υυυ

ms21g02.rl Stratagene ze03h12.sl Soares fet ze03h12.sl Soares fet zf16g10.sl Soares fet 5770 Arabidopsis thal

human STS WI-14071.

va53g01.rl Soares mou

21198 Arabidopsis tha zl31g06.sl Soares pre CK01713.5prime Drosop

Stratagene

zn55e09.rl

W94669 HSW6694 AA055104 AT5074 AA211548 AT50720 MMAA59917

000

OO

human STS WI-7527. zr95d02.sl Soares NbH

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5 25 85 71 7 7 7 7 71 85 32 108

AA221186 N97897

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AA185832 AA059032 MM4838 W36178 AA200846 AA200846

1131 1330 1104 1104 85

Homo sapiens

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Eukaryotae; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 396)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Hillier, L., Clark, N., Rucaba, T., Le, M., Lenon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R. WashU-Merck EST Project Unpublished (1995) human. Н DEFINITION ORGANISM TITLE JOURNAL COMMENT REFERENCE AUTHORS ACCESSION KEYWORDS RESULT SOURCE Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result

Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine

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polylinker; Site_1: Not 1; Site_2: Eco RI: 1st strand cDNA
was prepared from germinal B-cells (flow-sorted from
tonsils) provided by Dr. Louis Staudt of the NçI, and was
 ö
 Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (infoelmage.llnl.gov) for further information.
Seq primer: ml3 -40 forward
 Gaps
 33 aaattatgaaaagatttaaaaaaaaaaagatctcttataaaaaagaattcatcaaag 91
 Hiller L., Clark N., Dubuque T., Elliston K., Hawkins M., Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.;
 Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LLNL, contact the IMAGE Consortium (info@image.llnl.gov) for quality sequence stop: 173.
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 ö
 /clone_lib="Soares fetal liver spleen INFLS"
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Vertebrata, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 15-MAR-1997 (Rel. 51, Created)
15-MAR-1997 (Rel. 51, Last updated, Version 1)
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a 59 c 86 g 110 t
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Location/Qualifiers
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 Matches
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 FEATURES
 BASE CO
 RESULT ID HS:
AC AA.
NI 91
DT 15
DT 15
DE 2S
KW ES
 ŏ
```

```
Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector.Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4414 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fels. 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 173.
 12-MAR-1997
 Eukaryotze; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 233)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Huttan, M., Huttan, M., Huttan, M., Rucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Materston, R., Williamson, A., Wohldmann, P. and
 Gaps
 AA251633 233 bp mRNA EST 12-MAR-1997
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4A251.633
g1886597
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 2.9%; Score 22; DB 85; Length 233
larity 80.0%; Pred. No. 3.39e-04;
Conservative 0; Mismatches 8; Indels
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 The WashU-Merck EST Project
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WashU-Merck EST Project
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 TITLE
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 BASE COUNT
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 COMMENT
 RESULT
 Cp
g
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4

RESULT

Matches 69

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ORIGIN

DEFINITION

ACCESSION

RCE RGANISM

EYWORDS

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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1 (bases 1 to 424)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Thelsing,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 AA138421 424 bp mRNA EST 11-FEB-1997 mg88b09.r.1 Strategene mouse melanoma (#937312) Mus musculus cDNA clone 585785 5' similar to SW:DLDH_MYCGE P47513 LIPOAMIDE DEHYDROGENASE COMPONENT ;
mq71c01.rl Stratagene mouse melanoma (#937312) Mus musculus cDNA clone 584160 5' similar to SW:DLDH_BACSU P21880 LIPOAMIDE DEHYDROGENASE COMPONENT ;.
 Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Washington University School of MedicineP
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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 Pred. No. 3.39e-04;
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 312 ttgtttttggtgaagctacaattttagatcaa 343
 Contact: Marra M/Mouse EST Project
 Seq primer: primer name ambiguous High quality sequence stop: 382. Location/Qualifiers
 59 TIGCTITITGGICGCIAAAGITITIAGAICAA 90
 Waterston, R.
The WashU-HHMI Mouse EST Project
 73 g
 2.9%;
 Best Local Similarity 84.4%;
Matches 27; Conservative
 (bases 1 to 393)
 46 C
 Unpublished (1996)
 <1..>393
 Mus musculus
 Mus musculus
 house mouse.
 house mouse.
 MGI:358808
 91700622
 91683736
 AA138421
 EST.
 Mus.
 Query Match
 ω
 DEFINITION
 ORGANISM
 DEFINITION
 ORGANISM
 BASE COUNT
 TITLE
JOURNAL
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 REFERENCE
 AUTHORS
 ACCESSION
 AUTHORS
 mRNA
 REFERENCE
 KEYWORDS
 KEYWORDS
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 COMMENT
 RESULT
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 ô
 /organism="Mus musculus"
/organism="Wus musculus"
/organism="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dr. From M2
cells, a highly metastatic derivative of the K-1735
(mouse) melanoma. Average insert size: 1.0 kb; Uni-ZAP XR
Vector; -5 adaptor sequence: 5 GAATTCGGCACGAG 3 -3 adaptor sequence: 5 GAATTCGGCACGAG 3 -3 (clone="584160"
/clone="584160"
/dev_stage="M2 cells"
/dev_stage="M2 cells"
/lab_host="SOLR (kanamycin resistant)"
 Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Galsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,R., Steptoe,M., Tan,F., Underwook,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 ö
 Ä
 AA125483 393 bp mRNA EST 09-FEB-1997 mq71c01.rl Stratagene mouse melanoma (#97312) Mus musculus cDNA clone S84160 5' similar to SW:DLDH_BACSU P21880 LIPOAMIDE DEHYDROGENASE COMPONENT ;.
 Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
 Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 22-NOV-1996
 Gaps
 Gaps
 Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
1el: 314 286 1800
Fax: 314 286 1810
 ;
0
 ;
;
 Length 393;
 Length 233;
 Score 22; DB 49; Length 393
Pred. No. 3.39e-04;
...matches 5; Indels
 gattgctttaaattttgtattgaaacaaca-atacattttgcact 112
 633 GATTTCTTTAAGAATTGTATTGAAACCACCACCACCTTTTGCACT 589
 EST
 Score 22; DB 71; I
Pred. No. 3.39e-04;
0; Mismatches 8;
 Seq primer: -28ml3 revl ET from Amersham
 122 t
 312 ttgtttttggtgaagctacaattttagatcaa 343
 Contact: Marra M/Mouse EST Project
 59 TTGCTTTTGGTGTCGCTAAAGTTTTAGATCAA 90
 The WashU-HHMI Mouse EST Project
 High quality sequence stop: 382.
Location/Qualifiers
 73 g
 mRNA
 393 bp
 7.9%;
Local Similarity 84.4%;
Local 27; Conservative
 Query Match 2.9%;
Best Local Similarity 80.0%;
 (bases 1 to 393)
 46 c
 Conservative
 Unpublished (1996)
 1..393
 house mouse.
 Waterston, R
 MGI:358808
 a
 91683736
 AA125483
 36;
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Query Match

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BASE COUNT ORIGIN

source

FEATURES

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RESULT LOCUS

Email:

JOURNAL

TITLE COMMENT source

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Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT713 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."
 //organism="Homo sapiens"
//organism="Homo sapiens"
//orde="Vector: pTT3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; Ist strand cDNA
was prepared from germinal B-cells (flow-sorted from
tonsils) provided by Dr. Louis Staudt of the NCI, and was
then primed with a NotI - oligo(dT) primer [5'
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector.Library went
through one round of normalization, and was constructed by
 Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.,
Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,
Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,
Trevaskis E., Waterston K., Williamson A., Wohldmann P., Wilson R.;
"The Wash U-Merck EST Project";
 Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This Clone is a vailable royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seg primer: -41ml3 fwd. ET from Amersham High
 [5-MAR-1997 (Rel. 51, Created)
15-MAR-1997 (Rel. 51, Last updated, Version 1)
zs10b06.sl Soares NbHTGBC Homo sapiens cDNA clone 684755 3'.
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Length 427;
 8; Indels
 355 agtgcaaaatgtattgttg-tttcaatacaaaatttaaagcaatc 398
 589 AGTGCAAAAGGTGTGGGTGGTTTCAATACAATTCTTAAAGAAATC 633
 Seg primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 357.
Location/Qualifiers
 Score 22; DB 71; I
Pred. No. 3.39e-04;
0; Mismatches 8;
 /tissue_type="Germinal B-cell"
/lab_host="DH10B"
 /clone_lib="Soares NbHTGBC"
 /organism="Homo sapiens"
 BP.
 complement(<1..>427)
 Location/Qualifiers
 .T 8
HS1166232 standard; RNA; EST; 427
AA251305;
 Query Match 2.9%;
Best Local Similarity 80.0%;
 36; Conservative
 quality sequence stop:
 Homo sapiens (human)
 155 a
 Unpublished.
 q1886486
 source
 BASE COUNT
 -427
 Matches
 FEATURES
 ORIGIN
 δy
 ö
 This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:360433
 Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
 Homo sapiens

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;

Vartebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 427)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,

Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,

Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,

Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
 AA251305 427 bp mRNA EST 12-MAR-1997
zs10b06.s1 Soares NbHTGBC Homo sapiens cDNA clone 684755 3'.
AA251305.
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Gaps
 Washu-HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800
 0
 Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
 Score 22; DB 50; Length 424;
 Score 21; Luc...
Pred. No. 3.39e-04;
...artches 5; Indels
 Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 416.
Location/Qualifiers
1..424
 74 g 127 t
 Contact: Marra M/Mouse EST Project
 265 ttgtttttggtgaagctacaattttagatcaa 296
 The WashU-HHMI Mouse EST Project
 mouseest@watson.wustl.edu
 WashU-Merck EST Project
 Best_Local Similarity 84.4%;
Matches 27; Conservative
 2.98;
 48 C
 Unpublished (1996)
 Unpublished (1995)
 <1..>424
 Waterston, R.
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175 a

BASE COUNT ORIGIN

mRNA

Query Match

91886486

DEFINITION SSION

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RESULT

human.

SOURCE ORGANISM

WORDS

REFERENCE AUTHORS Wilson, R

The

TITLE JOURNAL

COMMENT

Gaps

1;

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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptco,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 mm69c03.rl Stratagene mouse macrophage (#937306) Mus musculus cDNA clone 533668 5' similar to gb:X65873 KINESIN HEAVY CHAIN (HUMAN);. AA072168
 1;
 ö
 This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 tycagaaagagtgaaagctttggagtcagccctgaaagaagccaaagaaaatgcatctcg 110
 591 TGCAAAAGGTGTGGGTTGTTTCAATACAATTCTTAAAGAAATCGAAGAGCGTGCACCTTT 650
 07-FEB-1997
 Gaps
 /clone_lib="Stratagene mouse macrophage (#937306)"
/dev_stage="WEHI-3 cell line"
/lab_host="SOLR (kanamycin resistant)"
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 ö
 ij
 Length 333;
 Length 427;
 Mismatches 34; Indels
 8; Indels
 355 agtgcaaaatgtattgttg-tttcaatacaaaatttaaagcaatc 398
Bento Soares and M. Fatima Bonaldo."
/clone="684755"
 complement(<1..>427)
155 A; 69 C; 60 G; 143 T; 0 other;
 Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
 Score 21; DB 32; Pred. No. 4.77e-03;
 Seq primer: -28m13 rev1 ET from Amersham
 Pred. No. 3.39e-04;
 /tissue_type="Germinal B-cell"
/lab_host="DH10B"
 Score 22; DB 85;
 0; Mismatches
 60 t
 /clone_lib="Soares NbHTGBC"
 /organism="Mus musculus"
 The WashU-HHMI Mouse EST Project
Unpublished (1996)
 Email: mouseest@watson.wustl.edu
 High quality sequence stop: 91. Location/Qualifiers
 mRNA
 93 g
 ô
 /clone="533668"
 2.7%; 5
ilarity 61.8%; F
Conservative
 2.9%;
larity 80.0%;
Conservative
 333 bp
 (bases 1 to 333)
 79 c
 Tel: 314 286 1800
Fax: 314 286 1810
 Local Similarity
tes 36; Conserv
 Mus musculus
 Local Similarity
nes 55; Conser
 house mouse.
 Waterston, R.
 MGI:320604
 BP;
 ø
 AA072168
 q1590513
 Sequence 427
 Query Match
 Query Match
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 6
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Matches
 51
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3']; double-stranded cDNA wasligated to Eco RI adaptors (GTTGGATTCGGTACC), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead."
 AM2201186 341 bp mRNA EST 12-FEB-1997 mp32501.rl Barstead mouse pooled organs MPLRB4 Mus musculus cDNA AA221186 AA221186
 Gaps
 Parkway,
 Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway Box 8501, St. Louis, Mo 63108 Tal: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through Linl.; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:430424 Seq primer: -28m13 rev2 ET from Amersham High quality sequence stop:
 Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T., Galsel S., Kucaba T., Lacy M., Le M., Martin J., Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B., Theising B., Wylle T., Lennon G., Soares B., Wilson R.,
 14-FEB-1997 (Rel. 50, Created)
14-FEB-1997 (Rel. 50, Last updated, Version 1)
my25c01.rl Barstead mouse pooled organs MPLKB4 Mus musculus cDNA
 /clone="696864"
/clone_lib="Barstead mouse pooled organs MPLRB4"
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 ö
 DB 108; Length 341;
 Score 21; DB 108; Length 34 Pred. No. 4.77e-03; 0; Mismatches 6; Indels
 mRNA <1..>341
Sequence 341 BP; 101 A; 67 C; 73 G; 100 T; 0 other;
 269 acaattgttaatgaaccataagaaatgtcttga 301
 383 ACAATTGTTAATGAGTAAGAACTAATGTCTTGA 351
 organism="Mus musculus"
111 agaccgtaaacgctatcagcaagaagtag 139
 "The WashU-HHMI Mouse EST Project";
 Location/Qualifiers
 651 AAAACGTAACGTTGATCAAGTAGAAGTAG
 /dev_stage="7 day"
/lab_host="DH10B"
 standard; RNA; EST; 341
 /strain="FVB/N"
 /sex="mixed"
 2.7%;
Sest Local Similarity 81.8%;
fatches 27; Conservative
 Mus musculus (house mouse)
 clone 696864 5'
 Waterston R.;
 Unpublished.
 T 10
MM1139719
 AA221186;
 Query Match
 q1840172
 RESULT 11
 DEFINITION
 source
 1-341
 Matches
 ACCESSION
 KEYWORDS
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COMMENT

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/note="Vector: Lambda ZAP II, Site_1: EcoR I; Site_2: Xho I: PolyA+ RNA, from asynchronous blood stage parasites of the Dd2 isolate cultured in vitro, was reverse transcribed using an oligo dT-Xho I primer. Second strand was prepared using RNase H and DNA polymerase I. EcoR I adapters were ligated to the cDNA, and it was digested with Xho I. Prepared fragments were ligated into EcoR I Xho I digested lambda ZAP II vector."

/clone="PF1470c"
 Avenida Antonio Carlos 6627, Belo Horizonte, MG, Brazil, 31270-010
 (bases 1 to 394)

Rabelo, E.M. L., Franco, G.R., Azevedo, V., Pena, H.B., Santos, T.M., Melra, W.S.F., Rodrigues, N.A., Ortega, J.M. and Pena, S.D.J. Analysis of CDNA libraries from different developmental stages of Schistosoma mansoni with the aim of producing Expressed Sequence
 Instituto de Ciencias Biologicas, Universidade Federal de Minas
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Platyhelminthes;
Trematoda; Digenea; Strigeidida; Schistosomatoidea;
Schistosomatidae; Schistosoma.
 Contact: Pena, H.B. and Pena, S.D.J. Laboratorio de Genetica-Bioquimica Laboratorio de Genetica-Bioquimica
 AA185832 394 bp mRNA EST 08-JAN-199 MAAD0115.MZR Schistosoma mansoni, adult worm (Pena, H.B. and Pena, S.D.J.) Schistosoma mansoni cDNA clone SMA0115 5' end. 4A185832
 Current status of the Plasmodium falciparum genome project Mol. Biochem. Parasitol. 79, 1-12 (1996)
97001675
 Length 358;
 4; Indels
 Department of Molecular Biology and Microbiology University of Central Florida Orlando, Fr. 32816-2360 Tel: 407 384 2061 Fax: 407 384 3095 Email: dchak@pegasus.cc.ucf.edu
 /organism="Plasmodium falciparum"
 Query Match 2.7%; Score 21; DB 1; Le Best Local Similarity 86.2%; Pred. No. 4.77e-03; Matches 25; Conservative 0; Mismatches 4;
 /organism="Schistosoma mansoni"
 /lab_host="E. coli XL-1 blue"
 84 t
 Tel: (5531)4415611
Fax: (5531)4415409
Email: heloisa@mono.icb.ufmg.br
 19 tgaaaaattagatgaacaattaaatgaac 47
 cocation/Qualifiers
 Contact: Debopam Chakrabarti
 47 9
 Seq primer: M13 Reverse.
Location/Qualifiers
 /strain="Dd2"
 Schistosoma mansoni
 43 c
 Unpublished (1996)
 <1..>358
 Seg primer: T3
 blood fluke.
 ď
 Imunologia
 Gerais
 source
 RESULT 13
 Source
 DEFINITION
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 BASE COUNT
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 1 (bases 1 to 341)
Marram M. Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Marram M., Hillier, L., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
 1 (bases 1 to 358)
Dame, J.B., Arnot, D.E., Bourke, P., Chakrabarti, D., Christodoulou, Z., Coppel, R., Comman, A., Craig, A., Fischer, K., Foster, J., Goodman, N., Hinterberg, K., Holder, A.A., Holt, D., Kemp, D., Lanzer, M., Lim, A., Newbold, C., Ravetch, J.V., Reddy, G.R., Rubio, J., Schuster, S.W., Su, X.-Z., Thompson, J.K., Vital, F., Wellems, T.E. and Werner, E.
 N97897 358 bp mRNA EST 18-NOV-1996
1470C3 czapPFDd2.1, Debopam Chakrabarti Plasmodium falciparum cDNA
clone PF1470C.
 ö
 Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
 Eukaryotae, mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Gaps
 Plasmodium falciparum
Eukaryotae; mitochondrial eukaryotes; Alveolata; Apicomplexa;
 /clone_lib="Barstead mouse pooled organs MPLRB4"
/sex="mixed"
/dev.stage="7 day"
/lab_host="DH108"
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800
Fax: 314 286 1810
 ó
 Length 341;
 Score 21; DB 52; Lengtn 34. Pred. No. 4.77e-03;matches 6; Indels
 Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
 Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 234.
Location/Qualifiers
 100 t
 269 acaattgttaatgaaccataagaaatgtcttga 301
 383 ACAATTGTTAATGAGTAAGAACTAATGTCTTGA 351
 /organism="Mus musculus"
/strain="FVB/N"
 The WashU-HHMI Mouse EST Project Unpublished (1996)
 73 g
 Haemosporida; Plasmodium.
 uery Match 2.7%;
st Local Similarity 81.8%;
ches 27; Conservative
 c 29
 malaria parasite.
 1..341
 Mus musculus
house mouse.
 MGI:430424
 q1674915
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12 LOCUS DEFINITION

RESULT

ORGANISM

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KEYWORDS

mRNA BASE COUNT

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08-JAN-1997

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<1..>408
 Unpublished.
 LT 15
MM4838
 source
 1-409
 mRNA
BASE COUNT
 Matches
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 /note="Vector: pBlueScript SK; Site_1: XhoI; Site_2: EcoRI; mRNA was extracted from adult worms and the library was constructed and excised according to the manufacturer's instructions (Uni-Zap XR vector,
 /clone_lib="Schistosoma mansoni, adult worm (Pena, H.B. and Pena, S.D.J.)"
 AA059032 408 bp mRNA EST 02-FEB-1997
2463a01.r1 Soares retina N2b4HR Homo sapiens cDNA clone 381576 5'.
4A059032
91551840
 ö
 Email: estéwatson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
INAGE Consortium (info@image.llnl.gov) for further information.
INAGE Length: 2135 Std Error: 0.00
Seq primer: -28M1 rev2 from Amersham
High quality sequence stop: 317.
Location/Qualifiers
 Eukaryotee: mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 408)
1 (bases I to 408)
1 Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Hiller, L., Huttan, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Waterston, K., Williamson, A., Wohldmann, P. and Wilson, R. Unpublished (1995)
 300 tgagcaacaactaatttgatcgtcaatatacaatccttcacatgtagttccacaaaa 356
 Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
 ;
0
 Score 21; DB 13; Length 394; Pred. No. 4.77e-03; 0; Mismatches 18; Indels
 /clone="381576"
/clone_lib="Soares retina N2b4HR"
/sex="male"
 Soares and M.Fatima Bonaldo."
 120 t
 /tissue_type="retina"
 /lab_host="DH5alpha"
 57 g
 /dev_stage="adult"
 /clone="SMA0115"
 Query Match
Best Local Similarity 68.4%;
Matches 39; Conservative
 Stratagene)
 56 c
 <1..>394
 ..408
 Homo sapiens
 161
 human.
 source
 RESULT 14
 BASE COUNT
ORIGIN
 DEFINITION
 ORGANISM
 TITLE
JOURNAL
COMMENT
 ACCESSION
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 AUTHORS
 mRNA
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KEYWORDS

FEATURES

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 Gaps
 30-APR-1996 (Rel. 47, Created)
04-MAR-1997 (Rel. 51, Last updated, Version 2)
ma84h03:r1 Soares mouse p3NMF19.5 Mus musculus CDNA clone 317429 5'
similar to SW:RS23_HUMAN P39028 40S RIBOSOMAL PROTEIN S23. [2]
PIR:S42105 ;
 Gaps
 Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, Mo 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality Possible reversed clone: similarity on wrong strand Seq primer: ETPrimer High quality sequence stop: 1. Rey
 Marra M., Hillier L., Allen M., Bowles M., Dietrich N.,
Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J.,
Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K.,
Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,
Waterston R.,
"The WashU-HHMI Mouse EST Project";
 Mus musculus (house mouse)
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 ;
0
 ;
0
 Score 21; DB 95; Length 409;
Pred. No. 4.77e-03;
 Length 408
 Minoru Ko (Wayne State University)."
/clone_11b="Soares mouse p3NMF19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
mRNA
<l...>409
Sequence 409 BP; 106 A; 87 C; 127 G; 89 T; 0 other;
 0; Mismatches 23; Indels
 0; Mismatches 13; Indels
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
 265 taattatacttcaaaatatttgacatctgctattatgccttctttag 311
 534 TAAGTCTAATGCTAAATATTTAACATTTGCTTCTAAGCTCGCTTTAG 488
 Score 21; DB 30;
Pred. No. 4.77e-03;
 /organism="Mus musculus"
 80 9
 standard; RNA; EST; 409
 Query Match 2.7%;
Best Local Similarity 65.7%;
Matches 44; Conservative
 Query Match 2.7%;
Best Local Similarity 72.3%;
 34; Conservative
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  - ŏ
    - 345 ctggagt 351 ||| || |263 ATGGTGT 269 qq
      - ŏ

Search completed: Fri Dec 5 08:12:53 1997 Job time: 266 secs.